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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                      Score
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Match
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1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT: *
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AAG75621
AAW77365
AAW37844
AAW37872
AAB24075
AAB24070
AAU08804
AAB72203
AAB72203
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(without alignments)
715.038 Million cell updates/sec
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Human ovarian tumo
Human colon cancer
zsig10 polypeptide
Human xkG growth f
Human protein comp
Secreted protein l
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                 Human PRO1030 prot
Breast cancer cell
Human huXAG-1/CCSG
Human secreted pro
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## ALIGNMENTS

RESULT 1
AAY73837
ID AAY7

AAY73837 standard; Protein;

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AAY73837;

14-MAR-2000 Human prostate tumor EST fragment derived protein #24 Claim 23; Page 318; 502pp; German. 04-NOV-1999 DE19820190-A1 Homo sapiens. treatment. Pancreas; tumor; EST; expressed sequence tag; human; cytostatic; proteins New human nucleic acid sequences from pancreatic tumors, and related proteins N-PSDB; Rosenthal A, Specht T, (META-) METAGEN GES GENOMFORSCHUNG MBH 28-APR-1998; 28-APR-1998; 1999-621386/54. DB; AAZ52865. (first entry) 98DE-1020190 98DE-1020190 Hinzmann B, Schmitt A, Pilarsky Ú, Dahl E;

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Best Local Similarity
This invention describes novel nucleic acid (cDNA) sequences (A) which have anticancer activity and are highly expressed in ovarian tumor tissue (and some also in testis and breast cancer tissue). The products of the invention can be used for gene therapy. (A) are used (i) for recombinant expression of polypeptides (B) and (ii) to isolate complete
                                                                                                        New nucleic acid sequences expressed tissues, and derived polypeptides, for identification of therapeutic agents
                                                                                                                                                                 WPI; 1999-591920/51.
N-PSDB; AAZ77486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes novel polypeptides and their encoding nucleic acids derived from human pancreatic tumor tissue which have cytostatic activity. The sequences are also useful in producing pharmaceutical compositions for treatment of pancreatic tumors. AAY73814-Y74252 represent protein fragments encoded by the human pancreatic tumor cDNA library derived expressed sequence tag (EST) sequences represented in
                                                                                Claim 25; Page 279; 310pp; German.
                                                                                                                                                                                                                                                                                    09-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ovarian
                                                                                                                                                                                                      Rosenthal A,
                                                                                                                                                                                                                               (META-) METAGEN GES GENOMFORSCHUNG MBH.
                                                                                                                                                                                                                                                           09-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                       Expressed sequence tag; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY76590 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             represent protein fragments encoded by library derived expressed sequence tag AAZ52858-Z53014.
                                                                                                                                                                                                                                                                                                              21-OCT-1999
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                                                                                                                                                                                                                                                                                                                                                                                           therapy;
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                                                                                                                                                                                                                                                                                                                                                                                           treatment
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Pred. No. 2.3e-108;
; Mismatches 0;
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treatment
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Best Local S
Matches 194
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                                                                                                                              Nucleic
                                                                                                                                                                                                                                                                                                                                                        29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                               28-SEP-2000; 2000WO-US26524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       colorectal carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human colon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genes. (B) are used (i) to identify agents suitable for treatment ovarian cancer; (ii) directly for treating this form of cancer
                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
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)B; AAH35026.
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                                                 Page 7865-7866;
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99US-0163280.
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                                                                                                                           colon cancer-associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis;
                                                                                                 sociated polypeptides, colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 194;
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AAH32943 to AAH37195 and

AAG73514

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AAG77788

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RESULT 4
AAW77365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression. For example, N and P may be used to treat disorders associated with decreased expression by rectrifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB7789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P
                                                                                                                                                                                                                                                            Human; mucous-mediated function; adhesion; tumour metastasis; bacterial colonisation; microbial infection; AIDS; cystic fibrosis; chronic obstructive pulmonary disease; asthma; Crohn's disease; sinonasal inflammatory disease; inflammatory bowel disease; bronchi
                                         Sheppard
                                                                                                                                                                    24-SEP-1998
                                                                                                                                                                                                                                                                                                                                        zsig10 polypeptide
                                                                                                                                                                                                                                                                                                                                                                         21-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW77365 standard; Protein;
N-PSDB; AAV59320
            WPI; 1998-531566/45
                                                                                                        19-MAR-1997;
                                                                                                                                       18-MAR-1998;
                                                                                                                                                                                                W09841627-A1
                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNMKKALKLLKTEL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QTLSRGWGDQLIWTQTYEEALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLA
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                                                                         ZYMOGENETICS
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                                                                                                        97US-0039631
                                                                                                                                       98WO-US05251
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100.0%;
                                                                           INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     175 AA
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Pred. No. 1.1e-101;
                                                                                                                                                                                                                                                               inflammatory bowel disease; bronchitis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated mucous-associated polypeptide, zsig10 - used to developroducts for treating e.g. tumour metastasis, microbial infections, cystic fibrosis, asthma, bronchitis or inflammatory bowel disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HuXAG-1; XAG; growth factor; colon cancer; t breast disease; liver disease; lung disease; wound healing; diagnosis; therapy; human.
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                                                                                                                                             Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
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                                                                        /note= "Claim
113..125
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138..150
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                                                                                                                                                                                                                                                                                                            = Epitope
"Claim 12"
                                                                                                                                                                                                                                                                                                                                                                                  # Mat_protein
"Claim 11"
                                                                                         Epitope "Claim 12"
                                                                                                                                                                 "Claim
                                                                                                                                                                 Epitope
"Claim 12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sig_peptide
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Pred. No. 1.8e-90;
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                                                                                                                                                                                                                                                                                                                                                           used to stimulate or promote liver regeneration, e.g. after surgery. They can also be used to prevent and heal damage to the lungs caused by various pathological states. They can be used to stimulate proliferation and differentiation and promote the repair of alveoli and bronchiolar epithelium to prevent, attenuate, or treat acute or chronic lung damage, e.g. emphysema, which results in the progressive loss of alveoli, and inhalation injuries, e.g. resulting from smoke inhalation and burns, that cause necrosis of the bronchiolar epithelium and alveoli. They can also be used to stimulate the proliferation and differentiation of breast tissue and could therefore be used to promote healing of breast tissue injury due to surgery, trauma or cancer. Antagonists can be used to treat hyperproliferative disorders, including cancer, in particular hepatocellular carcinoma, osteoclastoma, breast cancer, or colon cancer. The products can also be used for detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human growth factors also including huxaG-2 (see AAW37845) and huxaG-3 (see AAW37846). These proteins share homology with the C MAG protein of Xenopus laevis, which is involved in embryogenesis and is expressed in adult tissue. huxaG-1 is specifically found in cancerous colon cells and may therefore be a growth factor for colon cancer. huxaG-1 cDNA (see AAV19155) was isolated from a cDNA library derived from human colon cancer tissue. Vectors, host cells, antibodies, and screening methods for identifying agonists and antagonists of huxaG-1 are provided. HuxaG polypeptides are growth factors and can be used to stimulate proliferation of cells. They can be used to stimulate the proliferation and differentiation of chepatocytes to alleviate or treat liver diseases and pathologies such as fulminant liver failure caused by cirrhosis, liver damage caused by viral hepatitis and toxic substances. They can also be
                                                                                                                                                                                                                                                 Best
                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 1; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated human XAG growth factor(s) - used to develop products for treating e.g. liver, lung or breast diseases or hyperproliferative disorders, e.g. cancer.
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N-PSDB; AAV19155.
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                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                 MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE
                 DGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL 206
 DGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL
                                                                           ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP
                                                                                             ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP
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/note= "Claim 12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprises huxAG-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prises huXAG-1, a member of a novel family also including huXAG-2 (see AAW37845) and
                                                                                                                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                               Score 899; DB 19;
Pred. No. 1.8e-90;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                     Length 175;
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175
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RESULT 7
AAY59675
ID AAY5
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                                                                                                                                                                                                                                                  Query Match
Best Local Sim
Matches 175;
                                                                                                                                                                                                                                                                    This is the amino acid sequence of a novel human protein comprising a secretory signal isolated from stomach cancer cells. Its proteins can be used as nutritional sources or supplements. The proteins may also have cytokine functions, immune modulating functions, haematopoiesis regulating activity, activiny/inhibin regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PROT-)
 AAY59675 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPT; 1998-207380/18.
N-PSDB; AAV29047, AAV29048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human protein; secretory signal; nutritional source; immunity; haematopolesis; activin; inhibin; tumour; cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW37872 standard; Protein;
                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Pages 79; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 disorders, etc.
                                                                                                                                                                                                                                                                                                                                                                                                               Human proteins with secretory signal sequences - used to tre-
immune deficiencies, infections, tumours, and haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stomach cancer
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                                                                                                                                                      MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE
                                                                                                        ALYKSKTSNKPLMITHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP
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                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                               84.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 secretory signal amino
                                                                                                                                                                                                 Score 899; DB 17;
s; Pred. No. 1.8e-90;
 175
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Matches 175
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13-APR-1998;
10-AUG-1998;
04-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue types or cell species, as well as identifying tissue specific soluble proteins. The sequences can be used for chromosome mapping and identification of genes associated with hereditary diseases or drug response. Signal sequences from the cDNAs can be used in construction of secretion vectors. Other sequences derived from the extended cDNAs can be used to clone upstream genomic DNA sequences including promoters. This is in turn useful for identifying proteins that interact with promoter sequences. Some of the proteins may be useful in diagnosing and treating sequences. Some of the proteins may be useful in diagnosing and treating
                                                                                                                                                                                                                                                                                                                                                                                                                             several disorders including, but not limited to: cancer, hyperlipidaemia, cardiovascular and neurodegenerative disorders, autoimmune diseases, and rheumatic diseases, embryogenic disorders, hypertension, renal injury, amino acidurias, hypoglycaemia, male rat infertility and myopathies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            renal injury; amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prepare PCR primers and probes. These are useful for forensic matching positive identification by DNA sequencing. They may also be used in alternative fingerprint identification techniques. Antibodies against technical encoded by the extended cDNAs are useful in identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a human secreted protein of the invention. The extended cDNAs (or genomic DNAs obtainable from them) may be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Extended
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secreted
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                                                                                                                                                                                                                                                                                                                                                                               Sequence
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DGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL
                                                                               ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP
                                                                                                                                                                                          MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE
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                                                                                                                                                           MEKIPVSAFILLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE
                                                  ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP
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                                                                                                                                                                                                                                                                                                Similarity
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antibodies -
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98US-0081563.
98US-0096116.
98US-0099273.
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                                                                                                                                                                                                                                                                    Score 899; DB 20;
Pred. No. 1.8e-90;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                    Length 175;
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AAB24070
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30-NOV-1999;
20-DEC-1999;
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02-JUN-1999;
23-JUN-1999;
07-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; tumour; diagnosis; neoplastic disease; neoplastic cell growt proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosuppressive; immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; anglogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                       06-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammatory disorder; immunologic disorder.
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99US-0141037.
99US-0143048.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis; neoplastic disease; neoplastic cell growth;
tumourigenesis; identification; cancer; cytostatic;
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                                                                                                                                                                                                                                                                                                                                      99WO-US28313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence SEQ ID NO:40
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Thirty PRO polynucleotides encoding treatment, diagnosis and prevention of cancer PRO polypeptides, useful in

N-PSDB; AAC58380

2000-572270/53

Watanabe CK, Ashkenazi AJ,

Mood

WI;

Baker KP,

Goddard A,

Gurney AL,

Hillan KJ,

Roy MA;

Claim 61; Fig 28; 286pp; English.

CC one of the human PRO proteins designated PRO211, PRO290, PRO341, PRO335, CC PRO519, PRO717, PRO809, PRO809, PRO848, PRO943, PRO1005, PRO1009, CC PRO5195, PRO1009, PRO1009, PRO1009, PRO1009, PRO10111, PRO1153, PRO1182, PRO1182, PRO2004, CC PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO11710, PRO2094, CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell CC growth. The PRO polypeptides and nucleotides are useful in the CC treatment, diagnosis and prevention of cancer. The antibodies and other CC anti-tumour compounds maybe used to treat various conditions, including those characterised by overexpression and/or activation of the amplified CC progress. Exemplary conditions or disorders to be treated with such CC antibodies and other compounds include benign or malignant tumours CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours), CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours), CC epithelial, stromal and blastocoelic disorders, and inflammatory, CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR primers and hybridisation probes used in the isolation of the human PRO The present invention describes an isolated antibody that binds

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
The invention describes the novel use of a protein found in breast cancer cell membranes (BCMP 7) for diagnosing, preventing and treating breast cancers. The peptide has cytostatic action and potential uses in gene therapy and in vaccines. The polypeptide, antisense nucleic acids, or fusion proteins comprising and Green Fluorescent protein or the DsRR Fluorescent protein, antibodies specific for and/or nucleic acid are used for the prevention and/or treatment of breast cancer. Antibodies against may also be used for screening for and/or diagnosis of breast
                                                                                                                                        Diagnosing, cell membra
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Breast cancer cell membrane protein 7; BCMP 7; breast cancer;
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                                                                                                                                                                                                                                                                 25-FEB-2000; 2000GB-0004576
                                                                                                                                                                                                                                                                                           21-FEB-2001; 2001WO-GB00734.
                                                                                                                                                                                                                                                                                                                                                                                Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uences. AAC58367 to AAC58396 and AAB24057 to AAB240 polynucleotide and protein sequences given in the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP 151
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                                                                                                                                       nosing, preventing and membrane protein BCMP
                                                                                                                                                                                          2001-570651/64.
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                                                                                                              62pp;
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21..175
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                                                                                                                                                                                                                   Terrett JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC58396 and AAB24057 to AAB24089 represent human protein sequences given in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                   "Mature BCMP 7"
                                                                                                                                            treating
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Pred. No.
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                                                                                                                                                                                                                   Tyson KL;
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1.8e-90;
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This invention relates to a human growth factor polypeptide huXAG-1 also known as a colon cancer specific gene (CCSG). HuXAG-1 stimulates cell proliferation as a growth factor. The HuXAG-1 protein is useful for identifying compounds capable of enhancing or inhibiting cellular response induced by huXAG-1. The protein is also useful for stimulating proliferation of cells e.g. colon, breast, liver and lung cells, and hepatrocytes. It is useful for alleviating or treating liver diseases and pathologies such as fulminant liver failure caused by cirrhosis, liver damage caused by viral hepatitis and toxic substances, for preventing and treating damage to the lungs caused by various pathological states and for promoting healing of breast tissue injury due to surgery, trauma or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; growth factor; huxAG-1; colon cancer specific gene; (cell proliferation; liver disease; fulminant liver failure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB72203 standard; Protein;
                                                                                                                                                                                                                  Novel human growth factor polypeptide useful for diagnosing and treating colon cancer and liver diseases, to prevent and heal dithe lungs and for identifying modulators of therapeutic use -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB72203;
                                                                                                                                                                                       Claim 165; Fig 1; 59pp; English.
                                                                                                                                                                                                                                                                                                WPI;
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                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                      23-AUG-1996;
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175; Conser
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Pred. No. 1.8
0; Mismatches
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Matches 175
The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyp4 RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer. HuXAG-1 and the identified antagonist are useful for treating cancer, in particular colon cancer. Detecting altered levels of huXAG-1 and its polynucleotides are useful for diagnosing or detecting cancer in mammals. The gene encoding huXAG-1 is useful for monitoring human colorectal carcinoma. huXAG-1 nucleic acid molecules are also useful for
                                                                                                                                                                                           New nucleic acid that is a 5' expressed sequence obtaining cDNAs and genomic DNAs that correspond
                                                                                                                                                        Claim 13;
                                                                                                                                                                                                                                                                            Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                       06-SEP-2000
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                                                                                                                                                                                 diagnostic,
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                                                                                                                                                                                 forensic,
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llarity 100.0%;
Conservative
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                                                                                                                                                       ID 4190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expressed sequence
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                                                                                                                                                                                                                                                                                                                                  99US-0122487
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                                                                                                                                                                               gene therapy and chromosome mapping
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1.8e-90;
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Best Local :
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13-APR-1998;
10-AUG-1998;
04-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                         Extended specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 199
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Secreted protein; fingerprint identification commons applied; human; hereditary disease; diagnosis; cancer; chromosome mapping; human; hereditary disease; diagnosis; cancer; hyperlipidaemia; cardiovascular; neurodegenerative disorder; therapy; autoimmune disease; rheumatic disease; embryogenic disorder; myopathy; renal injury; amino aciduria; hypoglycaemia; male rat infertility;
The extended cDNAs (or genomic DNAs obtainable from them) may be used to prepare PCR primers and probes. These are useful for forensic matching or positive identification by DNA sequencing. They may also be used in alternative fingerprint identification techniques. Antibodies against the proteins encoded by the extended cDNAs are useful in identification of tissue types or cell species, as well as identifying tissue specific soluble proteins. The sequences can be used for chromosome mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  {\tt DNAS.~5'} ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream
                                                                                                                                                                                                                                                                                                                                                  Claim 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                       This sequence represents a human secreted protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-FEB-1999;
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DB; AAZ40846.
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                                                                                                                                                                                                                                                                                                                                          Page 240; 244pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132
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98US-0081563.
98US-0096116.
98US-0099273.
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Pred. No. 5.9e-64;
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RESULT 13
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identification of genes associated with hereditary diseases or drug response. signal sequences from the cDNAs can be used in construction of secretion vectors. Other sequences derived from the extended cDNAs can be used to clone upstream genomic DNA sequences including promoters. This is in turn useful for identifying proteins that interact with promoter sequences. Some of the proteins may be useful in diagnosing and treating several disorders including, but not limited to: cancer, hyperlipidaemia, cardiovascular and neurodegenerative disorders, autoimmune diseases, and rheumatic diseases, embryogenic disorders, hypertension, renal injury, amino acidurias, hypoglycaemia, male rat infertility and myopathles.
AAX41094 to AAX41347 represent 5' expressed sequence tags (ESTs) for human secreted proteins, and encode the proteins given in AAX12261 to AAX12514, respectively. The proteins given represent the signal peptide
                                                                                            New nucleic acids encoding human secreted proteins - ob cDNA libraries prepared from e.g. liver, ovary, brain, kidney, lung, umbilical cord, placenta and colon tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                 forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
                                                                  Claim 27;
                                                                                                                                                                                                      Duclert A,
                                                                                                                                                                                                                                                                  01-AUG-1997;
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les 117; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           secreted protein; EST; expressed sequence tag; diagnosis;
                                                                                                                                                           AAX41145.
                                                                                                                                                                                                                                    GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST secreted protein SEQ ID NO:343
                                                                  Page 682;
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                                                                                                                                                                                                      Dumas Milne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                    anti-inflammatory; tumour inhibition.
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                                                               824pp; English.
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                                                                                                                                                                                                      Edwards J,
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Pred. No. 2.3e-58;
0; Mismatches 9;
                                                                                                                                                                                                      Lacroix B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, receptor/ ligand activity, anti-inflammatory activity, receptor/ ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for procedures activity activity activity and activity and activity and activity are sequenced acids encoding the signal peptide can be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for obtaining activity activity activity and activity activity and activity and activity activity activity and activity and activity activity.
AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag (EST) sequences, corresponding to human secreted proteins. AAY64651 to AAY6448 represent the EST-related proteins corresponding to AAZ42265 AAZ43053. The 5' ESTs can be used for producing secreted human gene products. They can be used to identify and isolate 5' untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; 5' EST; expressed sequence tag; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability;
                                                                                                                                                                                                                                                                                                  09-APR-1998;
28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human 5' EST
                                                                                                                                  diagnostic,
                                                                                                                                                                                                 WPI; 2000-038446/03
                                                                                                                                                                                                                                                                                                                                                 09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY64672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY64672 standard; Protein;
                                                                                                                                                 Novel secreted protein 5' expressed
                                                                                                                                                                                                                                                                 (GEST
                                                                                                                                                                                                                                                                                                                                                                                 21-OCT-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                WO9953051-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regulation; identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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116; Conserv
                                                                                                                                                                                                                                 Milne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5' EST;
                                                                                                Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 AA;
                                                                                                                                  forensic,
                                                                                                                                                                                                                                 Edwards
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                604; 837pp; English.
                                                                                                                                                                                                                                                                                                98US-0057719
98US-0069047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide SEQ ID NO:833
                                                                                                                                  gene
                                                                                                                                                                                                                                 Duclert
                                                                                                                                therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 598;
Pred. No.
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                                                                                                                                  sequence tag sequences used and chromosome mapping proce
                                                                                                                                                                                                                                 Giordano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.2e-57;
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                                                                                                                                  procedures
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RESULT 15
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 Query Match
Best Local
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WPI; 1998-169093/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW37846 standard; Protein; 166 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                             W09807749-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-AUG-1998 (first entry)
                                Dillon PJ,
                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HuXAG-3; XAG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences used in the exemplification of the present invention
                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                23-AUG-1996;
                                                                                                                               22-AUG-1997;
                                                                                                                                                               26-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lung disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTD 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 MEKIPVSAFILLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        growth
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                              Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth factor; breast disease; liver disease;
emphysema; wound healing; cancer; diagnosis; therapy;
                                                                                              96WO-US13766
                                                                                                                               97WO-US14139
                                                                                                                                                                                                                                                            /note= "Claim 12"
104..115
                                                                                                                                                                                                                                                                                                           /label= Mat_protein
/note= "Claim 11"
25..44
                                                                                                                                                                                                                                                                                                                                                           /label- Sig_peptide
24..166
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor huXAG-3.
                                                                                                                                                                                                                                              /label=
                                                                                                                                                                                                                                                                                          /label- Epitope
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100.0%;
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; Pred. No. 4e-57;
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Matches Query Match

108;

Conservative

28; Mismatches Score 555; DB 1 Pred. No. 1e-52;

Local

Similarity

52.2%;

DB 19; 19;

Length 166; Indels

12;

Gaps

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caused by viral hepatitis and toxic substances. They can also be used to stimulate or promote liver regeneration, e.g. after surgery. They can also be used to prevent and head damage to the lungs caused by various pathological states. They can be used to stimulate proliferation and differentiation and promote the repair of alveoli and bronchiolar epithelium to prevent, attenuate, or treat acute or chronic lung damage, e.g. emphysema, which results in the progressive loss of alveoli, and inhalation injuries, e.g. resulting from smoke inhalation and burns, that cause necrosis of the bronchiolar epithelium and alveoli. They can also be used to stimulate the proliferation and differentiation of breast tissue and could therefore be used to promote healing of breast tissue injury due to surgery, trauma or cancer. Antagonists can be used to treat hyperproliferative disorders, including cancer, in particular hepatocellular carcinoma, osteoclastoma, breast cancer, or or colon cancer. The products can also be used for detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cells, antibodies, and screening methods for identifying agonists and antagonists of huXAG-3 are provided. HuXAG polypeptides are growth factors and can be used to stimulate proliferation of cells. They can be used to stimulate the proliferantian and differentiation of hepatocytes to alleviate or treat liver diseases and pathologies such as fulminant liver failure caused by cirrhosis, liver damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human growth factors also including huXAG-1 (see AAW3/844) and huXAG-2 (see AAW3/845). These proteins share homology with the XAG protein of Xenopus laevis, which is involved in embryogenesis XAG protein of Xenopus laevis, which is involved in embryogenesis.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This polypeptide comprises huXAG-3, a member of a novel fa human growth factors also including huXAG-1 (see AAW37844)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 3A-B; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated human XAG growth factor(s) - used to develop products for treating e.g. liver, lung or breast diseases or hyperproliferative disorders, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAV19157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is expressed in adult tissue. huXAG-3 cDNA (see AAV19157) was ated from a human small intestine cDNA library. Vectors, host
166 AA;
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41 LLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEEALYKSKTSN 100

LLLVTVSSNLA--IAIK-----KEKRP--PQTLSRGWGDDITWVQTYEEGLFYAQKSK

59

KPLMIIHHLDECPHSQALKKVFAENKEIQKLAE-QFVLLNLVYETTDKHLSPDGQYVPRI 159

KPLMVIHHLEDCQYSQALKKVFAQNEEIQEMAQNKFIMLNLMHETTDKNLSPDGQYVPRI 119

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GenCore version Copyright (c) 1993 - 2002

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Result
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C;Comment: This protein is C;Genetics: A;Gene: hAG-2

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76	76	76	76	76	76	76.5	76.5	78	78	78	78	78.5	78.5	78.5	78.5
7.1	7.1	7.1	7.1	7.1	7.1	7.2	7.2	7.3	7.3	7.3	7.3	7.4	7.4	7.4	7.4
1651	583	543	367	166	166	1025	985	1855	1853	1828	337	1570	1262	1033	917
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F88750	E75529	F64871	T39574	D86606	E72018	T10259	E69850	A59254	A46761	B59254	S06956	AC2012	I48855	A96714	T05430
protein vit-6 [imp	probable peptide A	oligopeptide-bindi	probable uracil ki	thioredoxin disulf	thioredoxin disulf	RNA-directed DNA p	formate dehydrogen	mysoin heavy chain	myosin heavy chain	mysoin heavy chain	segmentation prote	hypothetical prote	tripeptidyl-peptid	hypothetical prote	hypothetical prote

## ALIGNMENTS

Anterior gradient-2 - human C;Species: Homo sapiens (man) C;Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 21-Jul-2000

Biochem. Biophys. Res. Commun. 251, 111-116, 1998 A;Title: hAG-2, the human homologue of the Xenopus laevis A;Reference number: JE0350; MUID:99009231 A;Accession: JE0350

cement gland gene XAG-2,

C; Accession: JE0350 R; Thompson, D.A.; Weigel, R.J. JE0350

A;Molecule type: mrNA A;Residues: 1-175 <THO> A;Cross-references: GB:AF007791; NID:g3779196; PIDN:AAC77358.1; PID:g3779197

coexpressed with estrogen receptor (ER) in

breast cancer c

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hypothetical protein Y57A10A.u - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000 C;Accession: T31643 R.E.M. R.Smye, R.
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-186 <WIL>
A;Cross-references: EMBL:AL117195; PIDN:CAB55026.1; CESP:Y57A10A.u
A;Experimental source: clone Y57A10A
C;Genetics:
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                                                                                                                 A; Reference number: A; Accession: T31643
                                                                                                                                     submitted to the EMBL Data Library, September 1999 A; Reference number: Z21048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                   ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.6%; Score 899; DB 2; 1 ilarity 100.0%; Pred. No. 3.2e-74; Conservative 0; Mismatches 0;
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A;Gene: CESP:Y57A10A.u
A;Introns: 70/1
C;Superfamily: human a
R; Pearson, D.; Bowman, S.
submitted to the EMBL Data Library,
A; Reference number: S50917
A; Accession: S50919
A; Molecule type: DNA
A; Residues: 1-458 < PEA>
                                                                                                                                  hypothetical protein YMR191w - yeast (Saccharomyces N;Alternate names: hypothetical protein YM9646.03 C;Species: Saccharomyces cerevisiae C;Date: 10-Feb-1995 #sequence_revision 12-May-1995 #C;Accession: S50919; S55721
                                                                                                                                                                                                                                                           RESULT
S50919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Q1u, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functional delta R: Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-150 <MTH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A69000; MUID: 98037514 A; Accession: D69100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable protein disulfide-isomerase (EC 5.3.4.1) MTH1745 [similarity] - Methanobacterit
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Sep-2000
C;Accession: D69100
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les 35; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPLMIIHHLDECPHSQALKKVFAEN---KEIQKLAEQFVLLNLV--YETTDKHLSPDGQY 155
                                                                                                                                                                                                                                                                                                                                                                                                                                              SNKPLMIIHHLDECPHSQALKKVFAENKEIQ-KLAEQFVLLNLVYETTDKHLSPDGQY-V 156
: | : : | | | | | : : | | | | | |
TGKNVFMVFSASWCPACQKLESETLQNTEVQRRLAEDFIAVKIDVDTSPALSSRYRIYGV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPRLLFLDKN----GDLLQEFKNKKAEYKNYAYYYSSPADILNSMKDVLK 159
                                                                                                                                                                                                                                                                                                                                                                                                  PRIMFVDPS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEEALYKSKT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KPIFLLIHKSWCHACKALKKTFQQSNAKKAFKKLSEHFVMVNTEDDDEPFEEEYRPDGKY
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nilarity 27.1%;
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Pred. No. 1.1e-10;
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Pred. No. 0
                                                                                           January
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                                                                                                                                                               #text_change 04-Mar-2000
                                                                                                                                                                                                                                     cerevisiae)
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A;Cross-references: EMBL:Z47815; NID:9642280; PIDN:CAA87812.1; PID:9642283; MIPS: R;Gangloff, S.; McDonald, J.P.; Bendixen, C.; Arthur, L.; Rothstein, R. Wol. Cell. Biol. 14, 8391-8398, 1994
A;Title: The yeast type I topoisomerase Top3 interacts with Sgs1, a DNA helicase A;Reference number: A56359; MUID:95059068
A;Accession: S55721
                                                                                                                                                                                                                                            A; Experimental source: strain CWLO29
R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, CNucleic Acids Res. 28, 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumo A; Reference number: A81500; MUID:20150255
A; Accession: B81523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Kalman, S.; Mitchell, W.; Marathe, R.;
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia
A;Reference number: A72000; MUID:99206606
A;Accession: G72016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable disulfide bond isomerase - Chlamydophila pneumoniae (strains CWL029 C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
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A; Residues: 1-127, 'Y', 129-131, 'LALG', 136-249 <GAN>
A; Cross-references: EMBL: U22341; NID: 972677; PIDN
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                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-348 <ARN>
A;Cross-references: GB:AE001673; GB:AE001363; NID:g4377252; PIDN:AAD19071.1; PID:g437
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                                                                                                                        A;Cross-references: GB:AE002251; GB:AE002161; A;Experimental source: strain AR39, HL cells
                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-348 < REA>
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                                                                                                                      A; Experimental source: strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLIWTQTYEEALYK --- SKTSNKPLMI ---- IHHLDECPHSQ ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGTFSAPLSFLDPSLL--ADLDEMIRN--YKYE 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HVQPVALKKLSQKDINFIRNLELFKIMK - - TQNEVVDETSAYYMEKPGSYIEFTISEFNV
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Pred. No. 4
Score 87; 1
Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fan, J.; Olinger,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    not shown
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                                                                                                                                                    PIDN: AAF38711.1;
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                                                                                                                                                                                                                                                                                                    pneumoniae
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                                                                                                                                                                                                                                                                                                                                                     O.; Hicke
G.; Salzbe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIPS:YMR1
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                                                                                                                                                    PID:g718
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Local

Similarity

8.2%; 25.0%;

Conservative

26;

Mismatches

Indels

24;

Gaps

4

DB 2;

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RESULT 7
S19188
R; Sanders, G.; Lichte, B.; Mer
FEBS Lett. 311, 295-298, 1992
A:Title: cDNA encoding the ch
                                                                                          A:Molecule type: mRNA
A:Residues: 1-1688,'R','1690-1830 <ES2>
A:Experimental source: brain
A:Note: sequence extracted from NCBI backbone (NCBIN:121153, NCBIP:121154)
A:Note: the codon CGC for residue 1689 is inconsistent with the codon AGC
A:Accession: B44359
                                                                                                                                                                                                                                                                                                                                                                                                                       N;Alternate names: calmodulin-binding protein; myosin I heavy chain, 190K C;SpecLes: Gallus gallus (chicken)
C;Date: 31-Dec.1993 #sequence_revision 31-Dec.1993 #text_change 19-Jan-2001
C;Accession: S19188; A44359; B44359; S29249
R;Espreafico, E.M.; Cheney, R.E.; Matteoli, M.; Nascimento, A.A.; De-Camilli, submitted to the EMBL Data Library, Fabruary 1992
A;Description: Complete CDNA coding sequence of chicken brain p190, a calmodul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences
A;Reference number: A86491; MUID:20330349
A;Accession: C86607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disulfide bond isomerase [imported] - Chlamydophila pneumoniae C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change C;Accession: C86607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
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                                                          A; Molecule type: protein A; Residues: 155-164 <ES3>
                                                                                                                                                                                                                      A;Title: Primary structure and cellular localization of chicken brain A;Reference number: A44359; MUID:93107155
A;Accession: A44359
                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:Z11718
R;Espreafico, E.M.; Cheney, R.E.; Matteoli, M.; Nascimento, A.A.; De Camilli, P.V.; Lar J. Cell Biol. 119, 1541-1557, 1992
                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-1830 <ESP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myosin-V - chicken
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:BA000008; NID:g8979307; PIDN:BAA99141.1; GSPDB:GN00142 A;Experimental source: strain J138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-348 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEEALYKSKTSNKPLMIIHHLDEC--PHSQALKKVFAENKEIQKLAEQFVLLNLVY 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVAMEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YQEALQKSKEAELPLLVIFSGSDWNGPCMKIRKEVLESPEFIKRVQGKFVCVEVEY 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RCSLKQLKVLATLL - - - LSLSL - - - PTLEAAENRDS - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.2%;
  chicken ortholog
                                       Meyer, H.E.; Kilimann, M.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 87; L
Pred. No. 3.
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of the mouse dilute
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gene
product. Sequence
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R;Glaser, P.; Frang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-1151 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: AB1077;
A;Accession: AG1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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Best Local
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                                                                               1064
                                                                                                                                                             1021
                                       192
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                                                                                                                                                                                                                                                                                   50
                                   LDNMKKALKLLKT
                                                                               YRTSAKKISGYKLYQTPK
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                                       204
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D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F:645-666/Region: actin binding #status predicted F:765-909/Domain: neck #status predicted <NBC> F:912-1420/Domain: coiled coil #status predicted <COI> F:912-1420/Domain: carboxyl-terminal domain #status predicted F:169/Binding site: ATP (Lys) #status predicted F:1735/Binding site: phosphate (Thr) (covalent) #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable peptidoglycan bound protein (I
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;72-752/Domain: myosin motor domain homology <MMOT> F;163-170/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X67251; NID:g63364; PIDN:CAA47673.1; PID:g63365 C;Comment: The neck domain comprises six approximately 23-residue tandem C;Superfamily: myosin MYO2; myosin motor domain homology C;Keywords: actin binding; ATP; brain; coiled coil; nucleotide binding; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AL592022; PIDN:CAC97511.1; PID:g16414795; GSPDB:GN00178 A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-1142, 1144-1830 <SAN>
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A;Accession: S29249
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                                                                                                                                                                                961 VALDDSVAPVTVQYVDQNHKQIASPETLTGAYGEKFTAKQKKITNYTLVKTPANVSGTFN 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              567 KNKDTVYEEQIKVLKSSKKFKLLPELFQDEEKAISP 602
YETTDKHLSPDGQY-VPRIMFVDPSLTVRADITGRYSNR----LYAYEPADTALL----
                                                                                                                                                                                                                                        LARDTTVKPGAKK--DTKDSRPKLPQTLSRGWGDQLIWTQ-
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                                                             EKAQTVTFVYQKVTAGN--IIVDYVD-
                                                                                                                  EA------LYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVL---LNLV 141
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                                                                                                                                                                                                                                                                                                                               Score 84.5;
Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 85.5;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tierrez, A.; Vazquez-Boland, J.A.;
                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LPXTG motif) lin2283 [imported] - Listeria inno
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                                                                                                                                                                                                                                                                                                   51;
                                                             KNGEKLADSIVLTGKLNSS 1063
                                                                                                                                                                                                                                                                                                                                                       Length 1151;
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                                                                                                                                                                                                                                                                                                      67;
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Voss, H.; W
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K.D.; I
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hypothetical protein YLR176c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein L9470.18
C;Speclas: Saccharomyces cerevisiae
C;Date: 23-Feb-1995 #sequence_revision 12-May-1995 #text_change
C;Accession: $51421
R;Wohldmann, P.
                                                                                                                                                                                                                                                                                                                                                              C;Accession: T37859

R;Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, February 1996
A;Reference number: Z21750
A;Accession: T37859
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A;Experimental source: strain 972h-; cosmid c17G8
                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-217 <DEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable transcription factor - fission yeast (Schizosaccharomyces C;Species: Schizosaccharomyces nombe
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A; Residues: 1-771 <WOH>
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A; Accession: S51421
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                                                                                                                                            Local Similarity
nes 42; Conserv
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                                                                                                          14 HPSRRLTQG---
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les 47; Conserv
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                                 SRPKLPQTLSRGWGDQLIWTQTYEEALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENK 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D--TTVK------PGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEEALYKSKTSNKP 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSGSGP-------HPSRRLTQGR----WVRKSRVAMEKIPVSAFLLVALSYTLAR
                                                                       HTWRIFVEGVDGEDISKWVRK------VVFKL-----HDTYNNP---TRTIE
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 -EVIETGWGEFDIMVRIF---
                                                                                                                                                Conservative
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                                                                                                        --RWVRKSRVAMEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKD
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Pred No.
                                                                                                                                                               Score 83.5; Di
Pred. No. 4.1;
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-FAPEAHEKALTFYHHLKLHPYGPRMEEMKASGG 130
                                                                                                                                                Mismatches
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cell cycle protein kinase hsk1 - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-200
                                                                                                                                    R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Wedler, submitted to the EMBL Data Library, January 1999
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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A; Experimental source: strain 972h-;
     A;Cross-references: EMBL:AL035263; PIDN:CAB38417.1; GSPDB:GN00067; SPDB:SPBC776.12c
A;Experimental source: strain 972h-; cosmid c776
                                        A; Molecule type: DNA
A; Residues: 1~479 <LYN>
                                                                                               A; Reference number: Z21944
A; Accession: T40683
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A;Gene: F19K16.21
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A; Accession: C96829
A; Status: preliminary
                                                                           A; Status: preliminary; translated from GB/EMBL/DDB:
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A; Residues: 1-918 <STO>
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Pred. No. 24;
41; Mismatches
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cell cycle protein kinase hsk1 (EC 2.7.1.-) - fissi C;Species: Schizosaccharomyces pombe C;Date: 28-Oct-1995 #sequence_revision 10-Nov-1995 C;Accession: S56143; T40682 R;Masai, H.; Miyake, T.; Arai, K. EMBO J. 14, 3094-3104, 1995 A;Reference number: S56143; MUID:95347336 A;Accession: S56143
RESULT
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A; Residues: 1-507 < LYN>
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A; Accession: T40682
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A; Residues: 1-507 <MAS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      352
                 14
                                                                                                                                                                                                                                      83 LIWTQTYEEALYKSKTSNKP----LMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 LIWTQTYEEALYKSKTSNKP----LMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLL 138
                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                   RKRSI 494
                                                                                                  MKKAL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RKRSI 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNLAYEKKDDDTAFDNS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILWASCGSASIYKEKLRHKPSQEERLCLDFLEKCLELDCNKRISAE----EALDHDFLYL
                                                                                                                                   DNLAYEKKDDDTAFDNS--
                                                                                                                                                                  -NLVYETTDKHLSPDGQYVPRIMFVDPSLTVRADITGRYSNRLYAY---EPADTALLLDN 194
                                                                                                                                                                                                     ILWASCGSASIYKEKLRHKPSQEERLCLDFLEKCLELDCNKRISAE--
                                                                                                                                                                                                                                                                                                                                                                                          77/1; 359/1
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                                                                                                                                                                                                                                                                       28;
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                                                                                                                                   FGETSFEKDEDLTAKHLSHILDFKEQEETDEPTSLSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGETSFEKDEDLTAKHLSHILDFKEQEETDEPTSLSK 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 83;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or Tyr-specific protein kinases; protein kinase homol
                                                                                                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                                                                                                      Score 83;
                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                         В
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                                                                                                                                                                                                                                                                                                                                                                        protein kinases; protein kinase homol
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A; Experimental:
C; Genetics:
A; Gene: lplA
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C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: C70441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 01-Dec-2000
C;Accession: S29069; I66621
C;Accession: S29069; I66621
                                                                                                                                                                                                                                                                                                    R; Leahey, A.M.; Charnas, L.R
Hum. Mol. Genet. 2, 461-463,
A;Title: Nonsense mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus A;Reference number: A70300; MUID:98196666.
A;Accession: C70441
                                                                                                                                                  A; Gene: OCRL-1
                                                                                                                                                                      C; Genetics:
                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 883-912 <
                                                                                                                                                                                                                                                                                    A; Reference number: I54349;
                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A; Accession: S29069
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: The Lowe's oculocerebrorenal syndrome A; Reference number: S29069; MUID:92334430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Attree, O.; Olivos, I.M.; Okabe, I.; Bailey, Nature 358, 239-242, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-788 <A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Deckert, G.; Warren, P.V.;
                                                                                                                                                                                      A;Cross-references:
                                                                                                                                                                                                      A; Residues:
                                                                                                                                                                                                                                                A;Status:
                                                                                                                                                                                                                                                              A; Accession: 168621
                                                                                                                                                                                                                                                                                                                                                              A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
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                                55 TVKPGAKKDTKDSRPK--LPQTLSRGWGDQLIWTQTYEEAL-YKS----KTS-NKPLMII 106
                                                                                                                                                                                                                                            preliminary; translated
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TYKYDSKTDRWDSSGKCRVP----AWCDRILWRGTNVNQLNYRSHMELKTSDHKPVSAL 607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353-358, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49;
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                                                                                            Similarity
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                                                                          Conservative
                                                                                                                                                                                  <RES>
GB:S62085; NID:g385336;
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23.0%;
                                                                                                                                                                                                                                                                                                                                          L.R.;
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MUID:93278398
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                                                                                                                                                                                                                                                                                                                            1993
                                                                                                                                                                                                                                                                                                                                          Nussbaum, R.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
                                                                        Score 81.5; [Pred. No. 40; 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                from GB/EMBL/DDBJ
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                                                                                                                                                                                        PIDN: AAB26926.1;
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                                                                                                            DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
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                                                                        46;
                                                                                                            2;
                                                                                                                                                                                                                                                                                                      patients
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                                                                                                            Length 970;
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                                                                                                                                                                                        PID: g385337
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                                                                        Gaps
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Searc Job t	Ф	Qy	ФФ	Qy	В	ργ
th con	716	185	664	148	809	107
Search completed: October 9, 2002, 16:42:16 Job time : 23 secs	716 SKDSVTILNS 725	185 PADTALLLDN 194	DSQYCKPWLRAEPFE	148 -HLSPDGQYVPRIMFYDPSLTVRADITGRYSNRLYAYE 184	FHIGVKVVDERRYRKVFEDSVRIMDRMENDFLPSLELSRREFVFENVKFRQLQKGK 663	107 HHLDECPHSQALKKVFAENKEIQKLAE

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1063
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Copyright (c) 1993 - 2002 Compugen Ltd.
      DB
XAG_XENLA
NP77_XENLA
YM51_YEAST
MY5A_CHICK
RFXL_YEAST
YD67_SCHPO
OCRL_HUMAN
TOP2_PLANE
YM51_YEAST
ERA_HELP1
CBP1_ORYSA
AROE BACSU
TPP2_MOUSE
MY5A_RAT
MY5A_HUMAN
P021_NEAST
MY5A_HUMAN
P021_ROUSE
ITH3_RAT
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GM13_RAT
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Result No.

Database

Sequence:

Run on:

## ALIGNMENTS

PILA  REGIAN  RAG ZENIA  STANDARD; PRT; 183 AA.  P55868;  01-NOV-1997 (Rel. 35, Created)  01-NOV-1997 (Rel. 35, Last sequence update)  PALATIVE Secreted protein XAG precursor.  RAG.  RAG		Que Bes Bat	CC This SWISS-PR CC between the CC the European CC use by non- CC modified and CC entities requ CC or send an em	[1] SEQU TISS MEDL Sive Sive Sive ante Dev.	E 2 . 7 E	P55868; 01-NOV-1: 01-NOV-1: 01-NOV-1: Putative	G_X SUL
ment glan  dd (Probal)  AT HIGH  NP77 I.  183 /  Matrachia  dd (Probal)  AT Lute Plan  tute Plan  t	ALSYTLARDITVKPGAK 	2; AAB18819.1; POT 1 18 PUT 19 183 PUT 183 PUT 183 AA; 20475 MW; 9 183 AA; 20475 MW; 9 184 PUT 184	PROT entry is copyriq a Swiss Institute of a Bioinformatics Inst a r-profit institution b this statement is n quires a license agre amail to license@isb-	OM N.A.  It gland;  13224; PubMed=8850563  13224; PubMed=8850563	African cla coa; Chordat hia; Anura;	35, 35, 35,	'n
	TY TY EN 20	CRETED PROTEIN XAG. CBBDCE8 CRC64;  DB 1; Length 183; e-34; es 51; Indels 10;	6666	ment gland as a paradigm d (Probable). AT HIGH LEVEL IN CEMENT	rtebrata; Pipoidea;	nce update) ation update) ecursor.	183

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RESULT
NP77_XE
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YM51_YEAST
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15-JUL-1998
15-JUL-1998
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SIGNAL
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01-OCT-1996 (Rel. 34, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
Hypothetical 52.2 kDa protein in SGS1-
YMR191W OR YM9646.03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-Cement gland;
TISSUE-Cement gland;
Aberger F., Schueren C., Lepperding
Submitted (MAR-1997) to the EMBL/Ge
-I- SUBCELLULAR LOCATION: Secreted
-I- TISSUE SPECIFICITY: EXPRESSED A
                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Saccharom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-S288C
Pearson D., E
                           SEQUENCE FROM N.A
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                                                 NCBI_TaxID=4932;
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Bowman S.,
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36, Last annotation
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 Barrell
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the EMBL/GenBank/DDBJ databases.
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Pred. No. 9.7e-34;
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PUTATIVE SECRETED PROTEIN

AE3807C926044509 CRC64;
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 B.G.,
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SGS1-MRPL24 intergenic
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RESULT 4
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Gangloff S., McDonald J.P., Benedixen C., Arthur L., Roths
"The yeast type I topoisomerase Top3 interacts with Sys1,
helicase homolog: a potential eukaryotic reverse gyrase."
Mol. Cell. Biol. 14:8391-8398(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGD;
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STRAIN-W303;
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MEDLINE=93012002; PubMed=183040;
Sanders G., Lichte B., Meyer H.E., Kilimann M.W.;
"cDNA encoding the chicken ortholog of the mouse dilute
Sequence comparison reveals a myosin I subfamily with co
                                                                                                                                            Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                    TISSUE=Brain;
                                                               SEQUENCE FROM N.A.
                                                                                                                    Archosauria;
                                                                                                                                Eukaryota;
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                                                                                         NCBI_TaxID=9031;
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; U22341; AAB60288.1;
S0004803; YMR191W.
                                                                                                                                                                                                                                                                                                                  NGTFSAPLSFLDPSLL--ADLDEMIRN--YKYE
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20.1%;
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FVTW -> LALG (IN REF. 2).
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Pred. No. 1
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; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                   non-muscle) (Myosin
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Best Local
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-I. FUNCTION: PROCESSIVE ACTIN BASED MOTOR THAT CAN MOVE IN LARGE STEPS APPROXIMATING THE 36-NM PSEUDO-REPEAT OF THE ACTIN FILAME MAY BE INVOLVED IN MELANOSOME TRANSPORT, OR ALTERNATIVELY, IT MET REQUIRED FOR SOME POLARIZATION PROCESS INVOLVED IN DENDRITE PORMATION (BY SIMILARITY).

-I. SUBULIT: MAY BE A HOMODIMER, WHICH ASSOCIATES WITH MULTIPLE CALMODULIN OR MYOSIN LIGHT CHAINS.
                                                                                                                                                   DOMAIN
MOD_RES
CONFLICT
SEQUENCE
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DOMAIN
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DOMAIN
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Coiled o
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                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00015; IQ; 6.
SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00612; IQ; 6.
Pfam; PF00063; myosin_head; PRINTS; PR00193; MYOSINHEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X67251; CAA47673.1; -. EMBL; Z11718; CAA77782.1; -. HSSP; P08799; 1MMG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Espreafico E.M., Cheney R.E., Matteoli M., Node Camilli P.V., Larson R.E., Mooseker M.S.; "Primary structure and cellular localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01843; DIL;
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InterPro; IPR001609; myosin_head.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chains."
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FEBS Lett. 311:295-298(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93107155; PubMed=1469047;
TISSUE SPECIFICITY: NEURONAL AND NONNEURONAL CELLS OF THE BRAIN. SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN. SIMILARITY: CONTAINS 6 10 DOMAINS. SIMILARITY: CONTAINS 6 10 DOMAIN.
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27; Conserv
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
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ACTIN-BINDING (POTENTIAL).
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E -> EQ (IN REF. 2).
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                                                                   Mismatches
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0538B278DFC09F6E CRC64;
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YD67_SCHPO
Q10319;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFXL_YEAST P48743;
                                                                                                                                                                                                                                                                                                                                                Hypothetical SEQUENCE 8
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Saccharomycetales; Saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast)
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YLR176C OR L9470.18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                           1 Similarity
47; Conserv
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8 (Rel. 36, Last sequ
1 (Rel. 40, Last anno
al 90.6 kDa protein i
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25.7%;
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protein in CBF5-DKAl intergenic
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             PRT;
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01-OCT-1996 (Rel. 3
01-OCT-1996 (Rel. 3
14) 01-OCT-1996 (Rel. 3
                                                                                                                                                                                                                HSK1_SCHPO STANDARD; PRT; 5
P50582; 094678;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence up
16-0CT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A., Wals
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
-i-SIMILARITY: TO HUMAN AF9 AND ENL AND YEAST TRANSCRIPTION
INITIATION FACTOR TFIIF SMALL SUBUNIT (TFG3/ANC1).
                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fi. Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales; Schizosaccharomyces.
MEDIINE-95347336; PubMed-7621824;
Masai H., Miyake T., Arai K.-I.;
"hskl+, a Schizosaccharomyces pombe gene related to Saccharomyces cerevisiae CDC7, is required for chromosomal replication.";
                                                                                                                                                                                         Cell cycle protein kinase hskl (EC HSK1 OR SPBC776.12C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                SEQUENCE FROM N.A.
                                                                                                                              Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                    SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                            NCBI_TaxID=4896
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RESULT 8
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Best Local
                                                                         _HUMAN OCTALHUMAN STANDARD; PRY; OCTALHUMAN STANDARD; PRY; OU1968, Q15684; O60800; Q9UJG5; Q15774; Q9UMA5; O1-JUL-1993 (Rel. 26, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Inositol polyphosphate 5-phosphatase OCRL-1 (EC
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NP_BIND
BINDING
ACT_SITE
VARSPLIC
SEQUENCE
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PROSITE; PS50011; PROTEIN_KINASE_DOM;
Cell cycle; Cell division; Serine/thre
                      Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; Q16539; 1WFC.
InterPro; IPR000719; Euk_pkinase
InterPro; IPR002290; Ser_thr_pki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
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                                                               Homo sapiens (Human)
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SEQUENCE
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SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: REQUIRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. 14:3094-3104(1995).
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                                                                                                                                                                                                                                                                                                          -NLVYETTDKHLSPDGQYVPRIMFVDPSLTVRADITGRYSNRLYAY---EPADTALLLDN 194
                                                                                                                                                                                                                                                                                                                                   ILWASCGSASIYKEKLRHKPSQEERLCLDFLEKCLELDCNKRISAE----EALDHDFLYL
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                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A. (LONG AND SHORT FORM).
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129 129
216 216
92 119
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                                   Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                       58407
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                                                                                                                                                                                                                                                                                                                                                                                                 22.4%;
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ATP (BY SIMILARITY).
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                                      Craniata; Vertebrata; Catarrhini; Hominidae;
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3.7;
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                                      Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                       55;
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Zhang X., Hartz P.A., Philip E., Racusen L.C., Majerus F "Cell lines from kidney proximal tubules of a patient wisyndrome lack OCRL inositol polyphosphate 5-phosphatase accumulate phosphatidylinositol 4.5-bisphosphate."; 18101. Chem. 273:1574-1582(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
Mistry S.
                                                           VARIANTS LS GLN-500 AND GLN-524.

MEDLINE=98293952; PubMed=9632163;

Kawano T., Indo Y., Nakazato H., Shimadzu M., Matsuda I.

"Oculocerebrorenal syndrome of Lowe: three mutations in derived from three patients with different phenotypes.";

Am. J. Med. Genet. 77:348-355(1998).
                                                                                                                                      "Mutations are not uniformly distributed Mol. Gener uniforms.";
                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION.
MEDLINE-98104142;
                                                                                                                                                                                                                                                                                                                                                                        Zhang X., Jefferson A.B., Auethavekiat V., Majerus P
"The protein deficient in Lowe syndrome is a
phosphatidylinositol-4,5-bisphosphate 5-phosphatase.
Proc. Natl. Acad. Sci. U.S.A. 92:4853-4856(1995).
         Kubota T., S
Fukushima Y.
                                                                                                                                                                            VARIANTS LS TYR-375; GLN-500; FMEDLINE=98347141; PubMed=968221
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95281554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The Lowe's oculocerebrorenal syndrome gene encodes a homologous to inositol polyphosphate-5-phosphatase."; Nature 358:239-242(1992).
                              WARIANT LS ARG-522.
MEDLINE-99002770; F
                                                                                                                                                                                                                                           Lin T., Orr
Lewis R.A.,
                                                                                                                                                                                                                                                                           VARIANTS LS T-367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Nonsense mutations in the OCRL-1 gene oculocerebrorenal syndrome of Lowe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93278398;
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Lewis R.A., McInnes R.R., Nussbaum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Kidney;
MEDLINE=92334430;
                                                                                                                                                                                                                                 "Spectrum of mutations
                                                                                                                                                                                                                                                                 MEDLINE=97342912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leahey A.M., Charnas L.R., Nussbaum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Physical mapping
 Identification of two
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                                                                                                                                     Genet. Metab.
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.A., Nussbaum R.L.;
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                   Sakurai
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                             PubMed=9788721;
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                   Α.,
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                   Shimazu
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throughout the OCRL
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the OCRL1
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                                                                                                                                                                                                                                                                                                                                      P.W.;
                                                                                  the
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 VARSPLIC
VARIANT
                                                                                                     Hydrolase;
                                                                                                                                                                InterPro;
InterPro;
                                                                                                                                                                                      EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
MIM;
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 VARIANT
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                    VARIANT
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                                       VARIANT
                                                             VARIANT
                                                                                                                                                        Pfam;
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modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-slb.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis with ocular examination."
Mol. Genet. Metab. 69:213-222(2000)
-!- FUNCTION: CONVERTS PHOSPHATIDYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              families with Lowe syndrome."; Clin. Genet. 54:199-202(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          novel mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monnier N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20382695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20232168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20382695; PubMed=10923037;
Monnier N., Satre V., Lerouge E.,
"OCRL1 mutation analysis in French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roschinger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Carrier assessment in
                                                                                                                                                                                                                   TISSUE SPECIFICITY: BRAIN, SKELETAL MUSCLE, HEART, KIDNE LUNG, PLACENTA, AND FIBROBLASTS.
DISBASE: DEFECTS IN OCRL ARE THE CAUSE OF LOWE'S OCULOCE SYNDROME, A DISBASE CHARACTERIZED BY HYDROPHTHALMIA, CAT MENTAL RETARDATION, VITAMIN D-RESISTANT RICKETS, AMINOAC AND REDUCED AMMONIA PRODUCTION BY THE KIDNEY.
SIMILARITY: BELONGS TO THE INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE TYPE II FAMILY.
SIMILARITY: CONTAINS 1 GAP DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genet. Metab. 69:413-4440001.
FUNCTION: CONVERTS PHOSPHATIDYLINOSITOL 4,5-BISPHOSPHATE TO PHOSPHATIDYLINOSITOL 4-PHOSPHATE. ALSO CONVERTS INOSITOL 1,4
PHOSPHATIDITY TO THOSPHOT 1 4-RISPHOSPHATE AND INOSITOL 1,3
                                                                                         European Bioinformatics Institute.
                                                                                                                                                                              DATABASE: NAME=Lowe Syndrome mutation database;
WWW="http://www.nhgri.nih.gov/DIR/GDRB/Lowe/ocrll_mut_db.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRISPHOSPHATE TO INOSITOL 1,4-BISPHOSPHATE AND INOSITOL 1,3,4,5-TETRAKISPHOSPHATE TO INOSITOL 1,3,4-TRISPHOSPHATE. MAY FUNCTION LYSOSOMAL MEMBRANE TRAFFICKING BY REGULATING THE SPECIFIC POOL (
                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE PRODUCTS: 2 ISOFORMS; PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYSOSOMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHATIDYLINOSITOL 4,5-BISPHOSPHATE THAT
                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a
                                                                                                                the Swiss Institute
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PubMed=10767176;
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Pfam; PF00620; RhoGAP; 1 SMART; SM00128; IPPC; 1 SMART; SM00324; RhoGAP; J; M88162; AAA59964.1; ALT\_IN J; U57627; AAB03839.2; -... J; AL022162; CAA18150.1; -... J; AL022162; CAA18151.1; -... J; Z73496; CAA97842.1; -... J; S62085; AAB26926.1; -... 309000; PF00783; IPPc; IPR000300; Alternative 735 875 707 714 337 337 IPR000198; AAA59964.1; ALT\_INIT IPPC RhoGAP 1. splicing; Disease mutation GAP DOMAIN. (See http://www.isb-sib.ch/announce/ collaboration Loutstation n no way commercial

372 375

> 372 367 357

367 357

/FTId=VAR\_010169
G -> E (IN LOWE SY
/FTId=VAR\_010170
MISSING (IN LOWE SY
/FTId=VAR\_010171.
V -> G (IN LOWE SY
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SEQUENCE FROM N.A.
MEDLINE-94316496; PubMed-8041616;
MCAleese S., Goman M.,
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Eukaryota; Alveolata;
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                                                                                                                                                                             639 SKDSVTILNS 648
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nes 45; Conserv
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31, Last sequence update)
39, Last annotation update)
II (EC 5.99.1.3).
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23.7%;
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2; Mismatches
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Pred. No. 11;
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D -> G (IN LOWE
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H -> R (IN LOWE
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G -> E (IN REF. 3 AND 4).
; 90B6F6CDDD354BFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    A -> P (IN LOWE SYNDROME)
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/FTId=VAR_010176.
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R -> Q (IN LOWE SYNDROME)
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RESULT 10
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01-OCT-1996 (
16-OCT-2001 (
Hypothetical
Rhodococcus e
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Nucleic Acids Res. 22:2547-2551(1994).
-!- FUNCTION: CONTROL OF TOPOILOGICAL STATES OF DNA BY TRANSIENT
BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II
MAKES DOUBLE-STRAND BREAKS.
-!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
of double-stranded DNA.
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DOMAIN
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ACT_SITE
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SUBCELLULAR LOCATION: Nuclear.
-i- MISCELLANEOUS: EUKARYOTIC TOPOLSOMERASE I AND II CAN RELAX BOTH NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES RELAX ONLY NEGATIVE SUPERCOILS.
-i- SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
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-!- SUBCELLULAR LOCATION: Nuclear.
-!- MISCELLANEOUS: EUKARYOTIC TOPOISOME
                                                                                                                                                                                                                                                                                           1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00615; CCAATSUBUNTA. PRINTS; PR00418; TP1ZFAMILY. ProDom; PD000616; DNA_topoisoII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X79345; -; NOT_ANNOTATED_CDS. HSSP; P06786; 1BGW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                             1016 TLTTT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [somerase;
                                                                                                                                                                                                                                                                                                                                  189 ALLLDNMKKALKLLKTE
                                                                                                                                                                                                                                                                                                                                                                                                                                            140 LVYETTDKHLSPDGQYVPRIMFVDPSLTVRADITGRYS------NRLYAYEPADT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 WTQTYEEALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQ-----FVLLN 139
                                                                                                                                                                                                                                                                                        SYLISKLEKEKRIISNK 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WTQDYKEFLEELLTDEKHQLILDYIDNSSHEDICFTIKMDPAKLQKAEEEGLEKVFKLKS 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SM00433; TOP2c;
SM00434; TOP4c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR003957; CBFA_NFYB_topis.
IPR001241; DNA_topoisoII.
IPR002205; DNA_topoisoIV.
IPR003594; HATPase_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Topoisomerase: DNA-binding; ATP-binding; Nuclear protein.

144 149 ATP (POTENTIAL).

830 DNA CLEAVAGE (BY SIMILARITY).

271 281 POLY-ASN.

308 316 POLY-ASN.
                          (Rel. 32 Created)
(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
1 37.5 kDa protein in thcR 5'region
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                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 81.5; D
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POLY-LYS.
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5; Mismatches
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                                                                                                                                                                 PRT;
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                               (ORF6).
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RESULT 11
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Best Local S
Matches 31
                                                                                                                                                                                                                                                            YMS1_YEAST STANDARD; PRT; Q05050; O1-NOV-1997 (Rel. 35, Created) O1-NOV-1997 (Rel. 35, Last sequence 30-MAY-2000 (Rel. 39, Last annotat Hypothetical 93 3 kDa protein in T. YMRO31C OR YM9973.04C
                SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
Bowman S., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Degradation of the thiocarbamate herbicide dipropylcarbamothioate) and biosafening by F N186/21 involve an inducible cytochrome P-45
                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacclaromycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tamura T., Nagy I., Lupas A., Lottspeich F., Cejka Z., Schoof Tanaka K., de Mot R., Baumelster W.;
"The first characterization of a eubacterial proteasome: the complex of Rhodococcus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical SEQUENCE 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U26421; AAC45738.1; -.
EMBL; U17130; AAC45747.1; -.
InterPro; IPR004347; DUE245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dehydrogenase.";
J. Bacteriol. 177:676-687(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        YEAST
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Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPVTAVHHISHDPTLRA-TVALADGRELTGLALQRIYLDRV----DKFMSAEGNDDPRV- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSPDGQYVPRIM 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schoofs G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          339 AA;
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.., Baumeister W.;
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Best Local
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Q9ZLW0;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE-99120557; PubMed-9923682;

Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P. Alm R.A., Noonan B., Guild B.C., deJonge B.L., Carnel G., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carnel G., Tummino P.J., Caruso A:, Uria-Nickelsen M., Mills D.M., Ives C., Mills D.M., Wovis (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collar between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions
                                                                    entities requires a license agreement or send an email to license@isb-sib.cl
                                                                                                                                                                                                                 -!- FUNCTION: BINDS BOTH GDP AND GTP, HAS AN INTRINSIC GTPASE AND IS ESSENTIAL FOR CELL GROWTH (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ERA/TRME FAMILY OF GTP-BINDING
                                                                                                                                                                                                                                                                         gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical SEQUENCE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGD;
                         EMBL; AE001480; AAD06035.1; HSSP; P06616; 1EGA.
                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                             Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERA OR JHP0466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Last sequence up 16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z49213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
            InterPro;
                                                                                                                                              between
                                                                                                                                                                                                                                                                         "Genomic sequence comparison of two unrelated isolates jastric pathogen Helicobacter pylori.";
                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter
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                                                                                                                                                                                    SIMILARITY: CONTAINS 1 KH DOMAIN.
                                                                                                                                                                                                     PROTEINS. ERA SUBFAMILY
                                                                                                                                        SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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S0004633; YMR031C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPKLPQTLSRGWGDQLIWTQTYEEALYKSKTSNKPLMIIHHLDECPHSQALKKVFAE--- 124
                                                                                                                                                                                                                                                            c pathogen Helicobacter 397:176-180(1999).
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38; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NKEIQKLAEQFV - -
                                                                     an email to license@isb-sib.ch)
             IPR004087;
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Pred. No.
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                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                          There are no restrictions ong as its content is in
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                                                                                                  for
                                                                                                                                             collaboration
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RESULT 13
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Best Local :
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PROSITE; PS50
GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1994
01-0CT-1994
01-0CT-1996
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NP_BIND
NP_BIND
DOMAIN
SEQUENCE
PHAM: PF00450; Serine_Carbpept; 1.

PRINTS; PR00724; CRBOXYPTASEC.

PROSITE; PS00131; CARBOXYPEPT_SER_SER; 1.

PROSITE; PS00342; MICROBODIES_CTER; 1.

PROSITE; PS00560; CARBOXYPEPT_SER_HIS; 1.

Hydrolase; Carboxypeptidase; Glycoprotein; Zymogen; SIGNAL

PROPEP 26 36 POTENTIAL.

PROPEP 26 36 POTENTIAL.
                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                    Biochim. Biophys. Acta 1199:311-314(1994).
                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CV. YUKIHIKARI;
MEDLINE-94213891; PubMed-8161571;
Washio K., Ishikawa K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Last annotation update)
Serine carboxypeptidase I precursor (EC 3.4.16.5)
                                                                                                                                  MEROPS; S10.001;
                                                                                                                                                        EMBL; D17586; BAA04510.1; PIR; S43516; S43516.
                                                                                                                                                                                                                                                                                                                                                                              "Cloning and sequencing of the gene rice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa
                                                                                                      InterPro; IPR000379; Est_lip_thioest_actsite.
InterPro; IPR001563; Serine_carbpept.
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                                                                                                                                                                                                                                                                                                    SERINE CARBOXYPEPTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                               PTM: THREE DISULFIDE BONDS ARE PRESENT (POTENTIAL) SIMILARITY: BELONGS TO PEPTIDASE FAMILY S10; ALSO
                                                                                                                                                                                                                                                                                                                                          broad specificity.
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TE; PS50823;
                                                                                                                                               P08819;
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64
122
204
301
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(Rel. 30, Last sequence unit (Rel. 34, Last annotation)
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12 19
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23; KH_TYPE_
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125 G
280 K
34485 MW;
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27.8%;
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GTP (POTENTIAL).

GTP (POTENTIAL).

GTP (POTENTIAL).

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No. 4
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Matches 39
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ACT_SITE
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                                                                                                                                                    Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kobayashi Y., Mizuno
Sato T., Takeuchi M.;
Submitted (MAY-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AROD.
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01-OCT-1996 (Rel. 34, Last
16-OCT-2001 (Rel. 40, Last
Shikimate 5-dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bloinformatics Institute. There are no resti
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P54374;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus subtilis.
Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus/Staphylococcus
                                                                                                                                                                                         Aromatic
                                                                                                                                                                                                         InterPro; IPR002907; Shikimate_DH
Pfam; PF01488; Shikimate_DH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313
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93
                                     08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWA SIMILARITY: BELONGS TO THE SHIKIMATE DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mitted (MAY-1996) to CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATHWAY: FOURTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QTLSRG--WGDQLIWTQTYEEALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQK 130
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 GDKLVGYNTDGEGFVKSLMKVLDKPISELSFLMIGAGGAARAIFTTFVRNTPKKFDICNR 152
                                     GDQLIWTQTYEEALYKS -- KTSNKPLMIIHHL -----
                                                                           Similarity
39; Conser
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(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
-Achvdrogenase (EC 1.1.1.25).
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37.5%;
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Pred. No. 8.7;
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Pred. No. 4
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RESULT 15
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                                                                                                                                                                                                               Hydrolase;
ACT_SITE
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VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alternative splicing.";
Biochem. J. 304:517-523(1994).
-!- CATALYTIC ACTIVITY: Release of an N-terminal tripeptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
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STRAIN=LEADEN X A1;
MEDLINE=95091686; Po
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00136; SUBTILASE_
PROSITE; PS00137; SUBTILASE_
PROSITE; PS00138; SUBTILASE_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00082; Peptidase_S8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR000209; Peptidase_S8.
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SUBCELLULAR LOCATION: Cytoplasmic.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBTILASE FAMILY.
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AGSLTLSKTELGKKAGQSAAKRQGKFKKDVIPVHYYL-----IPPPTKIKNGSKDKE 1021
                                                 AGTLSGSGPHPSRRLTQGRWVRKSRVAMEKIPVSAFLLLVALSYTLARDTTVKPGAK---
                                                                                                                                     Similarity
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985 9
1262 AA;
                                                                                                                                                                                                                                      Alternative splicing.

44 44 CHARGE RELAY SYSTEM (BY SIMILARITY).

264 264 CHARGE RELAY SYSTEM (BY SIMILARITY).

49 449 CHARGE RELAY SYSTEM (BY SIMILARITY).

985 997 MISSING (IN SHORT ISOFORM).
                                                                                                            Conservative
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SUBTILASE_HIS; 1.
SUBTILASE_SER; 1.
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Last annotation update)
II (EC 3.4.14.10) (TPP-II) (Tripeptidyl
                                                                                                      31;
                                                                                                                                                                                                                  MW;
                                                                                                                               Score 78.5;
Pred. No. 31;
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DMDKQKSTLIDA
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        O9cquO mus musculu
O9581 homo sapien
O9na78 caenorhabdi
O9n587 caenorhabdi
O27777 methanother
O92485 rattus norv
O9af04 frankia sp.
O92952 listeria in
O92912 listeria in
O92918 caenorhabdi
                                                                                                          095994 homo sapien
088312 mus musculu
090y05 xenopus lae
042251 xenopus lae
096h50 homo sapien
09cqu0 mus musculu
                                                                                                                                                                                       Description
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## ALIGNMENTS

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RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             O95994 PRELIMINARY; PRT; 175 AA.
O95994;
01-MAY-1999 (TrembLrel. 10, Created)
01-MAY-1999 (TrembLrel. 10, Last sequence update)
01-DEC-2001 (TrembLrel. 19, Last annotation update)
SECRETED CEMBUT GLAND PROTEIN XAG-2 HOMOLOG (ANTERIOR GRADIENT (XENEPUS LAEVIS) HOMOLOG).
        Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF038451; AAC82614.1; -.
EMBL; AF007791; AAC77358.1; -.
EMBL; AF008867; AAF22484.1; -.
EMBL; BC015503; AAH15503.1; -.
                                                                                                                                                                                                                                                      MEDLINE-99009231; PubMed-9790916;
Thompson D.A., Weigel R.J.;
"hAG-2, the human homologue of the Xenopus laevis cement gland gene
XAG-2, is coexpressed with estrogen receptor in breast cancer cell
lines.";
                                                                                                                                                        SEQUENCE FROM N.A.
Zhang J.S., Smith D.I.;
"Human homolog of XAG is differentially expressed in tumors.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAG-2/R OR HAG-2/C
                                                                                                            TISSUE=COLON ADENOCARCINOMA;
                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 251:111-116(1998).
                                                                                                                                                                                                                                                                                                                                      TISSUE=BREAST;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
AA;
19979 MW;
F271B1BD377BEE11 CRC64;
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RESULT OR RESULT OF THE RESULT
                                                                                          RN [3]

RP SEQUENCE FROM N.A.

RY STRAIN-C57BL/6J; TISSUE-PANCREAS;

RC STRAIN-C57BL/6J; TISSUE-PANCREAS;

RX MEDLINE-21085660; PubMed-11217851;

RA KAWAI J., Shinagawa A., Shibarta K., Yoshino M., Itoh M., Ishii Y.,

RA KAWAI J., Shinagawa A., Shibarta K., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Ra Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Szauki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.

RA Szauki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.
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01-NOV-1998
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning of a gene, cells in mice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-INTESTINE;
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  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is coexpressed with estrogen
                                                     409:685-690(2001).
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the human homologue of the
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Pred. No. 4.1e-80;
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Sciurognathi; Muridae;
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annotation update)
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EMBL; AF044262; BAAC72705.1; --
EMBL; AK007677; BAB25181.1; --
EMBL; BC013334; AAH13334.1; --
                                                                                                                                                                                                                                                                                                                                            Q90Y05 PRELIMINARY; Q90Y05; Q90Y05; Q1-DEC-2001 (TrEMBLrel. 19, Create 01-DEC-2001 (TrEMBLrel. 19, Last s 01-DEC-2001 (TrEMBLrel. 19, Last a cement GLAND-SPECIFIC PROTEIN CGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
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                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Alexandrova E.M.,
                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-COLON,
                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                     Amphibia; Batrachia; Anura;
                                                                                                                                                                                                                                                                                                                                      Xenopus laevis (African clawed
                                                                                                                                                                                                                                                        laevis embryo.
                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8355
                                                                                                                                                                                                                                                                                                          Xenopodinae;
                                                                                                                                                                                                                                                              Three novel genes
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                                                                                                                                                                        32 MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE
                                                                                                                                                                                                    Local Similarity
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ENCE 175 AA; 19920 MW;
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                                                                                DGQYVPRIMEVDPSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL
                                                                                                                                                        METVLKSLFFLLVATSFTLAKE---
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                                                                                                                                                                                                                                                                                                                      Mesobatrachia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sive
                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
HYPOTHETICAL 19.2 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                               Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC008913; AAH08913.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-HEAD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Progressive determination during axis in Xenopus laevis."; Cell 58:171-180(1989).
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                                             PDGQYVPRIMEVDPSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL
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THKSWCGACKALKPKFAESTEISELSHNFVMVNLEDEEEPKHEDFSPDGGYIPRILFLDP
                      HHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKH--LSPDGQYVPRIMFVDP 164
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172 AA; 1
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50.68;
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X MEDLINE-21085660; PubMed-11217851;

X MEDLINE-21085660; PubMed-11217851;

X MEDLINE-21085660; PubMed-11217851;

X MEDLINE-21085660; PubMed-11217851;

X MEDLINE-21085660; PubMed-1217851;

X ARAMAN J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,

X Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

X A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

X A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Casavant T.,

X A Alzawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

X Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

X Kuehl P., Lewis S., Matsud T., Gissi C., King B., Kochiwa H.,

X Kuehl P., Lewis S., Matsud T., Nikaido I., Pesole G., Quackenbush J.,

X Kuehl P., Lewis S., Matsud T., Nikaido I., Pesole G., Quackenbush J.,

X Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

X Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

X Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

X Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

X Sakai K., Okido T., Bojunga N., Carninci P., de Bonaldo M.F.,

X Sakai K., Okido T., Bult C., Fletcher C., Fujita M., Gariboldi M.,

X Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

X Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
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Q9CQU0;
01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (APR-2001) to the EMBL EMBL, AK003481; BAB22811.1; -. EMBL; AK002862; BAB22413.1; -. EMBL; AK002862; BAB22413.1; -. EMBL; BC006857; AAH06857.1; -. MGD; MGI:1913323; 0610040B21Rik.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                               SNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNL--VYETTDKHLSPDGQYV 156
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1. 17, Last sequence update)
1. 19, Last annotation update)
1. 19 (RIKEN CDNA 0610040B21 GENE).
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Pred. No. 4e-
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thi; Muridae;
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                                      Q9NA78;
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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MEDLINE-96207227; PubMed-8619474;
MEDLINE-96207227; PubMed-8619474;
Andersson B., Wentland M.A., Ricafrente
"A 'double adaptor' method for improved
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Mammalia; Eutheria;
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Strausberg R.
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Catarrhini;
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G., Gibbs R.A.;
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shotgun library
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"Direct Submission.";
Submitted (JUL-2001) to the EMBL,
EMBL; AC006642; AAF39830.1; -.
Interpro; IPR000886; ER_target.
Interpro; IPR000063; Thiored.
PROSITE; PS00014; ER_TARGET; UNK)
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HYPOTHETICAL
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Science 282:2012-2018(1998).
EMBL; AL117195; CAB55026.1; -.
InterPro; IPR000063; Thiored.
SEQUENCE 186 AA; 21467 MW;
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Eukaryota; Metazoa; Nen
Rhabditidae; Peloderina
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Rhabditidae; Pel
NCBI_TaxID=6239;
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Eukaryota; Metazoa; Nematoda;
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STRAIN-BRISTOL N2
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MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                             "Genome sequence of the nematode C. elegans: a plinvestigating biology. The C. elegans Sequencing Science 282:2012-2018(1998).
                                                                    Waterston
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C. elegans c
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TREMBLIEL 05, 01-JAN-1998 (TREMBLIEL 05, 01-OCT-2001 (TREMBLIEL 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
EMBL: AE000930; AAB86215.1;
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Methanothermobacter.
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Pfam; PF00085; thiored; 1.
PROSITE; PS00194; THIOREDOXIN; UNKNOWN_1.
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                                                                                                     PTVIILDPS 129
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150 AA; 16939 MW;
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27.18;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 119; DB 17; Pred. No. 0.00071;
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Q924S5;
Q1-DEC-2001
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01-JUN-2001 (TremBLrel. 17, Last sequence update)
01-OCT-2001 (TremBLrel. 18, Last annotation update)
HYPOTHETICAL 78.0 KDA PROTEIN.
                                                                                                                                                                                             InterPro; IPR002543; FtsK_SpoIIIE.
Pfam; PF01580; FtsK_SpoIIIE; 1.
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
John T.R., Rice J.M., Johnson J.D.;
John T.R., Rice J.M., Johnson J.D.;
"Analysis of pFQ12; a 22.4 kb Frankia
Can. J. Microbiol. 0:0-0(2001).
EMBL; AY027524; AAK20150.1; -
                                                                                                                                                                                                                                                                                                                                                                                                Q9AF04;
01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                         Hypothetical protein; SEQUENCE 737 AA; 7
                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Actinobacteria; Act
Actinomycetales; Frankineae; Frankiaceae;
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-HLSPDGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPAD----TALLLDNMKK 197
                                                                                               LVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSR------GWGDQLIWTQTYEEA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VDNPIYLSDMGAALTGAESHEL--QDVLEETNILKRLYKALSLLKKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDPSL---TVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISRQLEVEPEGLEPEAENKQKSRRKLKRGKKEVGDELGAKPQLEMVTEA--TSDTSKEVL
                        ----TINNPLMIGRYRNTQPAEAHLRETYALVVGEQGSGKTNQLYVLTGQLARCTDVIV
                                               LYKSKTSNKPLMIIHHLDECPHSQALKKVFA---ENKEIQKLAEQFVLLNLVYETTDK-- 147
                                                                         LARFSEDLANDADLPAGAGVEV-----LPGTTRRSAVLEISTVDGFAEDLLFGDDYSEL 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MV--EVENVAHEDFQVTEEVKALTAEIVKTIRDIIALNPLYRESVLQMMQAGQRV-----
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                                                                                                                                    Similarity
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27.5%;
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Pred. No. 5.
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EMBL; AE00251; AAF38711.1; ---
EMBL; AP002548; BAA99141.1; ---
EMBL; AP002548; BAA99141.1; ---
 Q929J2;
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg White O., Hickey E.K., Peterson J., Utterback T., Berry Linher K., Weidman J., Khouri H., Craven B., Bowman C., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Elsen J., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Olinger L., Grimwood J., Davis R.W., Stephens R.S., "Comparative genomes of Chlamydia pneumoniae and C. Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CPN0933 OR CPJ0933 OR CP0928.
Chlamydia pneumoniae (Chlamydophila pneumoniae)
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-99206606; PubMed-10192388; Kalman S., Mitchell W., Marathe R., Lammel C., E Olinger L., Grimwood J., Davis R.W., Stephens R
                                  Q929J2
                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                               PHCI-2DPAGE; Q9Z6X3; TIGR; CP0928; -.
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20330349; PubMed=10871362;
                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20150255; PubMed-10684935;
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                                                                                                                                                   29 RVAMEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQT 88
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                                                                                          YQEALQKSKEAELPLLVIFSGSDWNGPCMKIRKEVLESPEFIKRVQGKFVCVEVEY 102
                                                                                                                                      RCSLKQLKVLATLL --- LSLSL --- PTLEAAENRDS
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sequence update)
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Salzberg S.L.,
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Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence up
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation
NUCLEAR RECEPTOR NHR-79 (FRAGMENT).
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                                                                                                                                      Eukaryota; Metazoa;
Rhabditidae; Pelode
                                                                                                                                                          Caenorhabditis elegans.
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NCBI_TaxID=1642;
                                                                                                                                                                                                                                                                                                                                                                               1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; SEQUENCE 1151 AA;
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"Comparative genomics of Listeria species.";
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Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O., Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P., Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D., Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G., Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H., Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R., Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A., Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
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Copyright (c) 1993 - 2002 Compugen Ltd.
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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US-08-9418-540-7
US-09-418-540-7
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US-09-418-540-7
US-09-613-6181-5
US-09-013-881-5
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US-09-08-313-185-53
US-09-08-313-185-53
US-09-08-5761A-53
US-09-08-761A-53
US-08-821-984-6
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5.544444444	1 US-08-306-473A-98 Sequence 1 US-08-201-660A-4 1 US-08-201-660A-4 1 US-08-209-762-98 Sequence 1 US-08-209-762-98 Sequence 2 US-08-473-344-98 Sequence 1 US-08-377-391A-2 Sequence 2 US-08-485-445A-98 Sequence 2 US-08-485-445A-98 Sequence 2 US-08-79-400-2 Sequence 2 US-08-79-162-98 Sequence 4 US-09-119-238-98 Sequence 4 US-09-093-539-98 Sequence 4 US-09-093-539-98 Sequence 5 PCT-US94-06931-4 Sequence 5 PCT-US94-06931-4 Sequence	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	
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US-08-306-473A-98 US-08-261-660A-4 US-08-262-762-98 US-08-473-344-98 US-08-473-344-98 US-08-474-303-6 US-08-485-445A-98 US-08-779-400-2 US-08-955-660-2 US-08-955-660-2 US-08-955-660-9 US-08-955-660-9 US-08-657-162-98 US-08-657-162-98 US-09-09-35-439-98 US-09-09-35-439-98 US-09-09-35-439-98 US-09-35-439-98 US-09-35-539-98 US-09-35-539-98 US-09-35-539-98 US-09-35-539-98 US-09-35-539-98 US-09-35-539-98 US-09-35-539-98	8 Sequence	ഗ	տ	4	4	4	4	4	ω	N	N	Ŋ	۲	1	1	1	_	-	ŀ
		PCT-US94-06931-4	PCT-US94-02465-98	US-09-395-453-2	US-09-146-620-2	US-09-093-539-98	US: 09-224-480-98	US-08-657-162-98	US-09-119-263-98	US-08-955-660-2	US-08-779-400-2	US-08-485-445A-98	US-08-377-391A-2	US-08-274-303-6	US-08-473-344-98	US-08-209-762-98	US-08-261-660A-4	US-08-306-473A-98	CO CO LAB FOR YOU
0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		Appli	Appl	Appli	Appli	App]	Appl	Appl	Appl	Appli	Appli	Appl	Appl:	Appli	Appl	Appl	Appli	Appl	

ALIGNMENTS

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RESULT 1
US-08-916-576B-2
US-08-916-576B-2
            TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08916576B Patent No. 6171816
                                                                                                                                                                                                       CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,347
FILING DATE: 23-AUG-1996
ATTORNEY/ACENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                 REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: I
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                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20005-3934
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DILLON, PATRICK J.
EBNER, REINHARD
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32 MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE 91

Query Match 84.6 Best Local Similarity 100 Matches 175; Conservative

84.6%;

Score 899; I

DB 4; .5e-96; s 0;

Length 175; Indels

0,

Gaps

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Mismatches

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RESULT 3
US-08-916-576B-8
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; NAME/KEY: SIGNAL
; LOCATION: -20...1
US-09-247-155-106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-10-04
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                                                                                                                                                                                         sequence 8, Application US/08916576B
Patent No. 6171816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 175; Conserv
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SOFTWARE: Patent.pm
SEQ ID NO 106
LENGTH: 175
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                                     GENERAL INFORMATION:
APPLICANT: YU, GUO-LIANG
APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Complementary DNAs FILE REFERENCE: GENSET.021A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bougueleret, Lydie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Duclert, Aymeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Dumas Milne Edwards, Jean-Baptiste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                     CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                     61 ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP
                                                                                                                                                                                                                                                                                                                                                                                                                         92 ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE 91
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STERNE,
                   ADDRESS:
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100.0%; Pr
  KESSLER, GOLDSTEIN & FOX, P.L.L.C
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                                                                                                    APPLICANT: DUMAS Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Complementary DNAS
FILE REFERENCE: GENSET.021A
CUBRENT APPLICATION NUMBER: U5/09/247,155A
CUBRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-08-10
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US-09-247-155-174
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                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 174, Application US/09247155A Patent No. 6312922
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COMPUTER RADDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release "1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36.688
REFERENCE/DOCKET NUMBER: 14.88
TREGISTRATION INFORMATION:
                     EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 VPRIMFVDPSLTVRADIXGRYGNRLYAYEPXDXPLLIXNMKKALKLLKTEL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 VPRIMFVDPSLTVRADITGRYSNRLYAVEPADTALLLDNMKKALKLLKTEL 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 AXXSNKPLMVIHHLEDCPYSQALKKVFAENXEIQELAQNFVMLNLVHETTDENLSPDGQY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 SKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSPDGQY 155
; ||||||:||:||:||:|||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 LGACLLLVALSXXLA-----XXXKGKDXRPIKGPQTLSRGWGDXIXWVQTYEEGLXK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.3%; Score 609.5; DB 4
71.3%; Pred. No. 1.9e-62;
tive 14; Mismatches 26
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Indels Length 170;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-916-576B-6
US-08-916-576B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08916576B Patent No. 6171816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity Matches 117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                             TELEFAX: (202) 371-254
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SIGNAL LOCATION: -20..-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: YU, GUO-LIANG
APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 131
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,347
FILING DATE: 23-AUG-1996
                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA:
              MOLECULE TYPE:
                                                                                                                               REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 DGQYXP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152
                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 XLXKSKTSNKPLMIIHHLDXCPHSQALKKXFAENKXIQKLAXQFVXLNLVYETTDKHLSP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92
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                                                                                                                                                                                   NAME: STEFFE, ERIC K. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                         CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                         FILING DATE:
                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGQYVP 157
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                                              amino acid
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                                                                166 amino acids
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              .protein
                                                                                                                371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YORK AVENUE, SUITE 600
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92.9%;
                                                                                                                                                                                                                                                                                                                                                         Release #1.0,
                                                                                                                                                                                                                                                                                                                         US/08/916,576B
                                                                                                                                                                                 36,688
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                                                                                                                                                                    1488.0500001
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Pred. No. 4.2e-62;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                         Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 131;
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Best Local Sim
Matches 108;
                                                                                                        Query Match
Best Local
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                                                                                           Matches
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                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                        NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE, DOCKET NUMBER: 141
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/024,347
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                   TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 LLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEEALYKSKTSN 100
 90 EEALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLA-EQFVLLNLVYETTDKH 148
                                                           39 AFLLLVALSYTLARDTTVKP---GAKKDTKDSRPKLP-----QTLSRGWGDQLIWTQTY 89
                                                                                                                                                                                                   STRANDEDNESS:
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                            SLVCLVLLCSALGEAVLKKPKKQAGTTDTKTDQEPAPIKTKGLKTLDRGWGESIEWVQTY 65
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                                                                                                        Similarity
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                                                                                                                                                                                                                                 183 amino acids
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DILLON, PATRICK
EBNER, REINHARD
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                                                                                                                                                                                     linear
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202) 371-2540
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                                                                                                    42.18;
49.48;
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                                                                                                                                                                                                                                                                                                                           1488.0500001
                                                                                                        Score 448; DB 4;
Pred. No. 8.6e-44;
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                                                                                           Mismatches
                                                                                           51;
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                                                                                                                    Length 183;
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RESULT 8
US-08-884-681-5
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Sequence 5, Application US/08884681
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                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024.
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OFERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACTION
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN &
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 172 amino acids
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                                                                                                                                                                 107 HHLDECPHSQALKKVFAENKEIQKLAEQFVLLNL--VYETTDKHLSPDGQYVPRIMFVDP 164
                                                                                                               165 SLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLL 202
                                                                                                                                                61 IHKSWCGACKALKPKFAESTEISELSHNFVMVNLEDEEEPKDEDFSPDGGYIPRILFLDP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                            2 ETRPRLGATCLLGFSFLLLVISSDGHNGLGKGFGDHIHW-RTLEDGKKEAAASGLPLMVI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSPDGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL 206
                                                                                 SGKVHPEIINENGNPSYKYFYVSAEQVVQGMKEAQERL 158
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                                                                                                                                                                                                                                                                                            20.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371-2600
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                                                                                                                                                                                                                                                                                            Score 222; DB 4; Length 172; Pred. No. 8.8e-18;
                                                                                                                                                                                                                                                                             Mismatches
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RESULT 9
US-09-258-643-5
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US-08-884-681-5
            Sequence 5, Application US/09258643
Patent NO. 6277373
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/884,681 FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                     476 TYKYDSKTDRWDSSGKCRVP-----AWCDRILWRGTNVNQLNYRSHMELKTSDHKPVSAL 530
                                                                                                                                                                                                           185 PADTALLLDN 194
                                                                                                                                                                                                                                                                                                                  531 FHIGVKVVDE----RRYRKVFEDSVRIMDRMENDFLPSLELSRREFVFENVKFRQLQKGK 586
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STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 7.7%; Score 81.5; Discord Similarity 23.7%; Pred. No. 1.6;
                                                                                                                                                                           SKDSVTILNS
                                                                                                                                                                                                                                             FQISNNGQVPCHFSFIPKLNDSQYCKPWLRAEPFEGYLEPNETV--DIS--
                                                                                                                                                                                                                                                                                -HLSPDGQ-----YVPRIM---
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Shah, Purvi
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Corley, Neil C.
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94.
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; Sequence 7, Application US/08560005

; Patent No. 6001354
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                                                                                                                                     GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 5:
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TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1420920
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                    APPLICANT: Pot, David A.
APPLICANT: Williams, Lewis T.
APPLICANT: Williams, Lewis T.
APPLICANT: Jefferson, Anne Bennett
APPLICANT: Majerus, Philip W.
TITLE OF INVENTION: No. 6001354el Grb2 Associating Protein and
TITLE OF INVENTION: Acids Encoding Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskett
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                               FQISNNGQVPCHFSFIPKLNDSQYCKPWLRAEPFEGYLEPNETV--DIS---
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23.7%;
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Pred. No. 1.6;
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                                                                                                                                                                                                                                                                                                                   RESULT 11
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                                                                                                                                                                                                                                                          Sequence 7, Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino a TOPOLOGY: lin
                                                                                                     APPLICANT: Pot, David A.
APPLICANT: Williams, Lewis T.
APPLICANT: Jefferson, Anne Bennett
APPLICANT: Majerus, Philip W.
TITLE OF INVENTION: No. 6296848el Grb2 Associating
TITLE OF INVENTION: Acids Encoding Therefor
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Reli
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Dow, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                         714 SKDSVTILNS 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       606 FHIGVKVVDE----RRYRKVFEDSVRIMDRMENDFLPSLELSRREFVFENVKFRQLQKGK 661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               551 TYKYDSKTDRWDSSGKCRVP----AWCDRILWRGTNVNQLNYRSHMLLKTSDHKPVSAL 605
                                                                                                                                                                                                                                                                                                                                                                                                                                               662 FQISNNGQVPCHFSFIPKLNDSQYCKPWLRAEPFEGYLEPNETV--DIS-----LDVYV 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Region LOCATION: 1..968 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.7%;
Local Similarity 23.7%;
es 45; Conservative
             CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 TVKPGAKKDTKDSRPK--LPQTLSRGWGDQLIWTQTYEEAL-YKS----KTS-NKPLMII 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                          PADTALLLDN 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -HLSPDGQ----YVPRIM-----
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6296848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   968 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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Pred. No. 1.8;
                                                Steuart Tower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
                                                    Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suite 2000
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US-09-534-638-5
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Best Local Similarity 23.7'
Matches 45; Conservative
                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Panula, Pertti A.J.
APPLICANT: Brandt, Annika
APPLICANT: Westerlund, Johanna
TITLE OF INVENTION: promoter for Neuropeptide FF Promoter and use thereof
TITLE OF INVENTION: for therapy and diagnosis
                CURRENT APPLICATION NUMBER: US/09/534,638
CURRENT FILING DATE: 2000-03-27
EARLIER APPLICATION NUMBER: 09/365755
EARLIER FILING DATE: 1999-08-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 5
LENGTH: 129
                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09534638 Patent No. 6320038
                                                                                                                                                                          FILE REFERENCE: 2530-104
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/560,005
FILING DATE: 17-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: DOW, KAIFED B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                              714 SKDSVTILNS 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 HHL-----DECPHSQALKKVFAENKEIQKLAE-------QFVLLNLVYETTDK-- 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 PADTALLLON 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        662 FQISNNGQVPCHFSFIPKLNDSQYCKPWLRAEPFEGYLEPNETV--DIS-----LDVYV 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 -HLSPDGQ-----YVPRIM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   606 FHIGVKVVDE----RRYRKVFEDSVRIMDRMENDFLPSLELSRREFVFENVKFRQLQKGK 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             551 TYKYDSKTDRWDSSGKCRVP----AWCDRILWRGTNVNQLNYRSHMLLKTSDHKPVSAL 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 TVKPGAKKDTKDSRPK--LPQTLSRGWGDQLIWTQTYEEAL-YKS----KTS-NKPLMII 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1. 968
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 14-OCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
COMPUTER: II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Region LOCATION: 1..968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H: 968 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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23.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 968;
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; TOPOLOGY: linear
; INMEDIATE SOURCE:
; LIBRARY: LUNGNOT
; CLONE: 1376382
US-09-013-881-5
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                                                                   Query Match
Best Local
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Best Local Similarity 22.9%;
Matches 16; Conservative
                                                  Matches
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APPLICANT: Bandma
                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                          NAME: BILLINGS, LUCY J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF TELECOMMUNICATION INFORMATION: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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ADDRESSEE: Incyte Ph
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                25 VRKSRVAMEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLI 84
                                                               Local
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CITY: Palo Alto
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                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                 TYPE:
                                                                                                                                                                                                                                                                                             TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
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                                                                                                                                                                                                                           LENGTH:
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                                               tch 7.3%; Score 78; DB 4; Length 453 al Similarity 22.5%; Pred. No. 1.5; 45; Conservative 34; Mismatches 79; Indels
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                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                             453 amino acids
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3174 Porter Drive
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Corley, Neil C.
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;; Pred. No. 0.23;
14; Mismatches
                                                                                                                                                                                                                                                                                                                                              PF-0470
                                                                                                                                                                                                                                                                                                                                              SD
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                                                  79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
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RESULT 15
US-08-313-185-53
; Sequence 53, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
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                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein PCT-US92-05401-4
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PCT-US92-05401-4
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APPLICANT: Lemischka, Ihor R.
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                                                                                                                                                                                                                                                                                                                      Query Match
Best Local !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:

NAME: Feit, Irving N.

REGISTRATION NUMBER: 28,601

REFERENCE/DOCKET NUMBER: LEM-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: IMCLONE SYSTEMS INCORPORATED STREET: 180 VARICK STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1160 amino acids
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                                                                                                                                                      1000 LGLLSPQAQVEDSRNNLVLRTSSLHLSLTGCRLPK 1034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 LRKGGFYSQKVTTNPNLRIISLNTNLYYGPNIMTLNKTDP----
                                                                                                                                                                                                                            952 RPSFP-NLTSFLGCQL---ADAEEAMYQN------VDGRVSECPHTYQNRRPFSREMD 999
                                                                                                                                                                                                                                                 68 RPKLPQTLSRGWGDQLIWTQTYEEALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKE 127
                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: NEW YORK
                                                                                                                                                                                                                                                                                                  Local Similarity es 27; Conserv
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                                                                                                                                                                                                                                                                                                ; Score 78; DB; Pred. No. 5.8; 17; Mismatches
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Search completed: October Job time: 19 secs
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                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodimer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 1. MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                               145
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                                                                                                                                                                                                                                                                                                      211 GPNHS-PLSAAAAIRTFRMGMNDEETVA---LIAGGHTLGKTHGAGPASHVGPPEAAPIE 266
                                                                          379 THRDMGPKRYIGPEVPKEDLIWQDPPQYPTEDIILKAAIAASGLVSELVSAWASAST 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                       97
                                                                                                                                                                                                                                                                                                                                     12 GPHPSRRLTQGRWVRKSRVAMEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKL 71
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                                                                                                                                                                                                                                                                 72 PQTLSRGWGD-----
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                                                                                                                                                  APDIIPDPFDPSKKRKPTMLVTDLLRFDPEYEKISRRFLNDPEFEAFARAW-----FKL 378
                                                                                                             TDKHLSPD----GQYVPR--IMFVDPSLTVRADI-----TGRYSNRLYAYEPADT 188
                                                                                                                                                                                     -----KTSNKPLMIIHHLDEC-PHSQALKKVFAENKEIQKLAEQFVLLNLVYET 144
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Zhang, Ying
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Breast cancer cell
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Human XAG growth f
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Human ovarian tumo
Human colon cancer
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	AAM40426	22	109	3.4	7	3
	AAC04178	22	105	ນ ນ • •	7	41
	AAM91788	22	105	3.4	7	40
	AAM86554	22	73	3.4	7	39
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	AAB58921	21	39	6.8	14	26
	AAY11939	20	56	8.3	17	25
	AAM24502	22	168	11.7	24	24
	AAU07647	22	166	11.7	24	23
	AAB31192	22	166	11.7	24	22
	AAB72205	22	166	11.7	24	21
	AAU25728	22	166	11.7	24	20
	AAB00194	21	166	11.7	24	19
	AAW37846	19	166	11.7	24	18
	AAY76568	20	89	٠	29	17
	AAY11882	20	62		42	16
	AAY11881	20	56		55	15
	AAY59718	20	131		59	14
	67	21	115	55.8	115	13
	AAY12312	20	116		116	12

## ALIGNMENTS

RESULT 1 AAY73837

AAY73837 standard; Protein; 206

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14-MAR-2000

(first entry)

AAY73837;

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Claim 23; Page 318; 502pp; German.
                                          WPI; 1999-621386/54.
N-PSDB; AAZ52865.
                                                                                                                                                                                                                Human prostate tumor EST fragment derived protein #24
                proteins
                        New human nucleic acid sequences from pancreatic tumors,
                                                                                                     28-APR-1998;
                                                                                                                     28-APR-1998;
                                                                                                                                      04 - NOV - 1999
                                                                                                                                                       DE19820190-A1:
                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                        treatment.
                                                                                                                                                                                               Pancreas; tumor; EST; expressed sequence tag; human; cytostatic;
                                                                  Rosenthal A, Specht T,
                                                                                   (META-) METAGEN GES GENOMFORSCHUNG MBH
                                                                                                    98DE-1020190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel polypeptides and their encoding nucleic acids derived from human pancreatic tumor tissue which have cytostatic activity. The sequences are also useful in producing pharmaceutical compositions for treatment of pancreatic tumors. AAY73814-Y74252 represent protein fragments encoded by the human pancreatic tumor cDNA library desived expressed sequence tag (EST) sequences represented in AAZ52858-Z53014.
         This invention describes novel nucleic acid (cDNA) sequences (A) which have anticancer activity and are highly expressed in ovarian tumor tissue (and some also in testis and breast cancer tissue). The products of the invention can be used for gene therapy. (A) are used (1) for
                                                                                          New nucleic acid sequences expressed in ovarian, tissues, and derived polypeptides, for treatment identification of therapeutic agents
                                                                                                                                                     WPI; 1999-591920/51.
                                                                                                                                                                            Rosenthal A,
                                                                                                                                                                                                                         09-APR-1998;
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genes. (B) are used (i) to identify agents suitable for treatment of ovarian cancer; (ii) directly for treating this form of cancer (including expression from gene therapy vectors) and (iii) for generatior of specific antibodies. (A) are identified by assembling ESTs (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTs from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. AAVT6505-Y7658 represent protein fragments encoded by the human ovarian tumor cDNA library derived EST fragments represented in AAZT7450-Z77572.
                                                                                                                                                                                    29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                      05-APR-2001
                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                                                                    03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG75621 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                   useful for preventing,
                                                               Nucleic acids encoding
                                                                                                                                  Ruben SM,
                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                         28-SEP-2000; 2000WO-US26524
                                                                                                                                                                                                                                                                               WO200122920-A2
                                                                                                                                                                                                                                                                                                                                   colorectal carcinoma
                                                                                                                                                                                                                                                                                                                                                Human; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                         Human
                                                                                                                                                                                                                                                                                                                                                                                                                              AAG75621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 DNMKKALKLLKTEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 PHPSRRLTQGRWVRKSRVAMEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLP
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                                                                                                                                                                                                                                                                                                        sapiens
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                                                                                           AAH35026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194
                                                                                                                                  Barash SC,
                                                                                                                                                                                                                                                                                                                                                                        cancer antigen
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                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                     99US-0157137.
99US-0163280.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194
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100.0%;
                                                                                                                                                                                                                                                                                                                                                colon
                                                   4277 human
diagnosing
                                                                                                                                  Birse
                                                                                                                                                                                                                                                                                                                                                cancer antigen;
                                                                                                                                                                                                                                                                                                                                                                        protein SEQ ID
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Pred. No.
                                                                                                                                  CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                 colon cancer-associated polypeptides,
and/or treating colorectal cancers -
                                                                                                                                  Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 20; 1
2.9e-182;
                                                                                                                                                                                                                                                                                                                                                                           NO:6385
                                                                                                                                                                                                                                                                                                                                                diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 194;
                                                                                                                                                                                                                                                                                                                                                  detection;
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Claim 11;

Page 7865-7866;

AAH32943 to AAH37195 and

AAG73514 9803pp;

to AAG77788 English

represent

human colon

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AAW77365
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW77365 standard;
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N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
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      WPI; 1998-531566/45.
N-PSDB; AAV59320.
                                                                                        Sheppard
                                                                                                                                                                                                                                                                                                                                                                                        WO9841627-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; mucous-mediated function; adhesion; tumour metastasis; bacterial colonisation; microbial infection; AIDS; cystic fibrosis; chronic obstructive pulmonary disease; asthma; Crohn's disease; sinonasal inflammatory disease; inflammatory bowel disease; bronchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      zsig10 polypeptide
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                                                                                                                                                                                                             19-MAR-1997;
                                                                                                                                                                                                                                                                    18-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                  ) ZYMOGENETICS
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                                                                                                                                                                                                                                                                    98WO-US05251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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AAW37844
ID AAW3
AAW37844
AAW37844
AAW3
AC AAW3
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AAW3784
AAW37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated mucous-associated polypeptide, zsigl0 - used to develop products for treating e.g. tumour metastasis, microbial infections, cystic fibrosis, asthma, bronchitis or inflammatory bowel disease \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUXAG-1; XAG; growth factor; colon cancer; tumour marker;
breast disease; liver disease; lung disease; emphysema;
wound healing; diagnosis; therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW37844 standard; Protein; 175
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                                                               Peptide
                                                                                                                           Peptide
                                                                                                                                                                                          Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 82; 109pp; English.
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/label= Epitop
/note= "Claim
138..150
                                                                                                                                                                                               /note=
61..72
                                                             /label= Epitope
/note= "Claim 12"
113..125
                                                                                                                                                 /label= Epitope
/note= "Claim 12"
                                                                                                                                                                                                                                                                                                        /label= Epitope
                                                                                                                                                                                                                                                                                                                                                 /note= "Claim 11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                          /label= Epitope
                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                        /label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.0%;
                                                                                                                                                                                                                 "Claim
                                                                                                                                                                                                                                                                                 "Claim 12"
                    Epitope
"Claim 12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 175; DB 19;
Pred. No. 1.2e-163;
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                                                                                                                                                                                                            Matches 175;
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                                                                                                                                                                                                                                                                                                                                                                                            caused by viral hepatitis and toxic substances. They can also be used to stimulate or promote liver regeneration, e.g. after surgery. They can also be used to prevent and heal damage to the lungs caused by various pathological states. They can be used to stimulate proliferation and differentiation and promote the repair of alveoli and bronchiolar epithelium to prevent, attenuate, or treat acute or chronic lung damage, e.g. emphysema, which results in the progressive loss of alveoli, and inhalation injuries, e.g. resulting from smoke inhalation and burns, that cause necrosis of the bronchiolar epithelium and alveoli. They can also be used to stimulate the proliferation and differentiation of breast tissue and could therefore be used to promote healing of breast tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        huxAG-3 (see AAW37846). These proteins share homology with the XAG protein of xenopus laevis, which is involved in embryogenesis and is expressed in adult tissue. huxAG-1 is specifically found in cancerous colon cells and may therefore be a growth factor for colon cancer. huxAG-1 cDNA (see AAV19155) was isolated from a cDNA library derived from human colon cancer tissue. Vectors, host cells, antibodies, and screening methods for identifying agonists and antagonists of huxAG-1 are provided. HuxAG polypeptides are growth factors and can be used to stimulate proliferation of cells. They can be used to stimulate the proliferation and differentiation
                                                                                                                                                                                                                                                                                                                               injury due to surgery, trauma or cancer. Antagonists can to treat hyperproliferative disorders, including cancer, particular hepatocellular carcinoma, osteoclastoma, breas or colon cancer. The products can also be a second cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated human XAG growth factor(s) - used to defor treating e.g. liver, lung or breast diseases or hyperproliferative disorders, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9807749-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of hepatocytes to alleviate or treat liver diseases and pathologies such as fulminant liver failure caused by cirrhosis, liver damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           huxAG-3 (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 1; 141pp; English.
                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This polypeptide comprises huXAG-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-169093/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-AUG-1996;
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 121
                                                                     61
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                                                                                                                                        Local Similarity
                                                                ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP 151
DGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV19155
                                                                                                                                                                                                                                                                              175 AA
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                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factors
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/note= "Claim 12"
                                                                                                                                                                                                                            85.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                               products can also be used for detection
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                                                                                                                                                                                                            0,
                                                                                                                                                                                                                            Score 175; DB 19;
Pred. No. 1.2e-163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a member of a novel family of huxAG-2 (see AAW37845) and
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                                                                                                                                                                                                                                                                                                                                                                                   Antagonists can
                                                                                                                                                                                                                                          Length 175;
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                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                  breast cancer,
                                                                                                                                                                                                                                                                                                                                                                 in
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RESULT 6
AAW37872
RESULT 7
AAY59675
ID AAY59675 standard; Protein; 175
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                                                                                                                                                                                                  Matches
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Best Local
                                                                                                                                                                                                                                                                   This is the amino acid sequence of a novel human protein comprising a secretory signal isolated from stomach cancer cells. Its proteins can be used as nutritional sources or supplements. The proteins may also have cytokine functions, immune modulating functions, haematopoiesis regulating activity, activity, inhabin regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity.
                                                                                                                                                                                                                                                                                                                                                                                                         Human proteins with secretory signal sequences - used to treat immune deficiencies, infections, tumours, and haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human protein; secretory signal; nutritional source; immunity; haematopoiesis; activin; inhibin; tumour; c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW37872 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Pages 79; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-207380/18.
N-PSDB; AAV29047, AAV29048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stomach cancer cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chemokinetic; thrombolytic; anti-inflammatory; inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW37872;
                                                                                                                                                                                                                                                                                                                                                                                               disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kato S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PROT-) PROTEGENE INC. (SAGA) SAGAMI CHEM RES CENTRE.
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                                                                                                                                                                                                                                               Sequence
                                                           121
                                                                                 152
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                                                          MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE
                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                               etc.
                                                                                                                                                                                                                                               175 AA;
                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                            100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   secretory signal amino acid sequence
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                                                                                                                                                                                                              Score 175; pred. No.
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                                                                                                                                                                                                             DB 19; 1
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Matches 175
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13-APR-1998;
10-AUG-1998;
04-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                           secretion vectors. Other sequences derived from the extended cDNAs can be used to clone upstream genomic DNA sequences including promoters. This is in turn useful for identifying proteins that interact with promoter sequences. Some of the proteins may be useful in diagnosing and treating several disorders including, but not limited to: cancer, hyperlipidaemia, cardiovascular and neurodegenerative disorders, autoimmune diseases, and rheumatic diseases, embryogenic disorders, hypertension, renal injury, amino acidurias, hypoglycaemia, male rat infertility and myopathies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a human secreted protein of the invention. The extended cDNAs (or genomic DNAs obtainable from them) may be used to prepare PCR primers and probes. These are useful for forensic matching or positive identification by DNA sequencing. They may also be used in alternative fingerprint identification techniques. Antibodies against the proteins encoded by the extended cDNAs are useful in identification of tissue types or cell species, as well as identifying tissue specific soluble proteins. The sequences can be used for chromosome mapping and identification of genes associated with hereditary diseases or drug response. Signal sequences from the cDNAs can be used in construction of secretion wenters.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secreted protein; fingerprint identification technique; chromosome mapping; human; hereditary disease; diagnosis; cancer; hyperlipidaemia; cardiovascular; neurodegenerative disorder; therapy; autoimmune disease; rheumatic disease; embryogenic disorder; myopathy;
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                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                           MEKIPVSAFILLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE
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DGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL
                                                                       ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP
                                               ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         injury; amino aciduria; hypoglycaemia;
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                                                                                                                                                                                                                                                                          Similarity
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98US-0081563.
98US-0096116.
98US-0099273.
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                                                                                                                                                                                                                                                                          Score 175; DB 20;
Pred. No. 1.2e-163;
                                                                                                                                                                                                                                               Mismatches
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175
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RESULT 8
AAB24070
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                                                                                                                                                                                                    proliferation; tumourigenesis; identification; cancer; cytostatic; noottopic; neuroprofective; antiinflammatory; immunosuppressive; immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; angiogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB24070 standard;
06-JAN-2000;
                                                                                           WO200053755-A2
                                                                                                                                                                              inflammatory disorder; immunologic disorder.
                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                                                                                 tumour;
2000WO-US00376
                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                            diagnosis; neoplastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
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                                                                                                                                                                                                                                                                                                                       identification;
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                                                                                                                                                                                                                                                                                                                                            neoplastic cell growth;
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02-JUN-1999; 23-JUN-1999; 07-JUL-1999; 26-JUL-1999; 30-NOV-1999; 20-DEC-1999; 05-JAN-2000; 08-MAR-1999; (GETH \_ GENENTECH INC 99WO-US12252. 99US-0141037. 99US-0143048. 99US-0145698. 99WO-US28313. 99WO-US28313. 99WO-US05028

Ashkenazi AJ, Watanabe CK, Wood Baker KP, ΨI; Goddard Α, Gurney AL, Hillan KJ, Roy MA

N-PSDB; AAC58380 2000-572270/53.

Thirty PRO polynucleotides encoding treatment, diagnosis and prevention O. PRO polypeptides, useful cancer in the

Claim 61; Fig 28; 286pp; English

PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1132, PRO1182, PRO1184, PRO1281, PRO1281, PRO2198, PRO33, PRO834, PRO8317, PRO1170, PRO2094, PRO2145 OR PRO2198, PRO antagonists can be used to inhibit tumour cell growth. The PRO polypeptides and nucleotides are useful in the treatment, diagnosis and prevention of cancer. The antibodies and other canting the conditions of the antibodies and other compounds maybe used to treat various conditions, including those characterised by overexpression and/or activation of the amplified PRO genes. Exemplary conditions or disorders to be treated with such cantibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukaemilas and lymphoid malignancies, other disorders such as neuronal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR primers and hybridisation probes used in the isolation of the human PRO one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009 The present invention describes an isolated antibody that binds PRO535

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RESULT 9
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Best Local :
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        The invention describes the novel use of a protein found in breast cancer cell membranes (BCMP 7) for diagnosing, preventing and treating breast cancers. The peptide has cytostatic action and potential uses in gene therapy and in vaccines. The polypeptide, antisense nucleic acids, or fusion proteins comprising and Green Fluorescent protein or the DSRe Fluorescent protein, antibodies specific for and/or nucleic acid are used for the prevention and/or treatment of breast cancer. Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences. AAC58367 to PRO polynucleotide and the present invention.
                                                                                                                            Diagnosing, preventing cell membrane protein !
                                                                                                                                                                                                                                                                                                                                                                   Key
Peptide
                                                                                                     Claim
                                                                                                                                                             N-PSDB;
                                                                                                                                                                                              Boyd RS,
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DB; AAS13480.
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may also
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                                                                                                    Fig 1; 62pp; English.
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21..175
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screening
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Best Local S
Matches 175
This invention relates to a human growth factor polypeptide huxAG-1 also known as a colon cancer specific gene (CCSG). HuxAG-1 stimulates cell proliferation as a growth factor. The HuxAG-1 protein is useful for identifying compounds capable of enhancing or inhibiting cellular response induced by huxAG-1. The protein is also useful for stimulating proliferation of cells e.g. colon, breast, liver and lung cells, and hepatocytes. It is useful for alleviating or treating liver diseases and pathologies such as fulninant liver failure caused by cirrhosis, liver damage caused by viral hepatitis and toxic substances, for preventing and treating damage to the lungs caused by various pathological states and for promoting healing of breast tissue injury due to surgery, trauma or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer in a patient. The method for monitoring/assessing breast treatment in a patient and for the identification of metastatic, cancer cells in samples from a patient. This sequence is breast cancer cell associated protein 7 (BCMP 7), encoded by a gene loc chromosome 7p21.3, described in the method of the invention.
                                                                                                                                                                                      Claim 165; Fig 1;
                                                                                                                                                                                                                Novel human growth factor polypeptide useful for diagnosing an treating colon cancer and liver diseases, to prevent and heal the lungs and for identifying modulators of therapeutic use -
                                                                                                                                                                                                                                                                                N-PSDB;
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DB; AAF63314.
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175; Conser
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid that is a 5' expressed sequence tag (5' EST) obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and diagnostic, forensic, gene therapy and chromosome mapping produced the control of the contr
                                                                                                                                                                                                                    The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 years prepared from total human RNAs or polyA+ RNAs derived from 30
                    N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL
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175; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5' EST;
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                                                                                                                                                                                                                                                                                                                                                           SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
therefore be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000EP-0200610
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                                                                                                                                                                                                                                                                                                                                                           ID 4190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ŗ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.0%; 50
100.0%; Pr
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Pred. No.
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obtain
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1.2e-163;
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                                                                                                                                                                                                                                                                                                                                                                                                                    mapping procedures
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RESULT 12
AAY12312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                       human secreted proteins, and encode the proteins given in AAY1261 to AAY12514, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein secreted action sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell
                                                                                                                                                                                        New nucleic acids encoding human secreted proteins - obtained cDNA libraries prepared from e.g. liver, ovary, brain, prostatkidney, lung, umbilical cord, placenta and colon tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
                                                                                                                                                                                                                                                                                                                                                      01-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human 5' EST secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY12312 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNAs. 5' ESTs are also used in diagnostic,
                                                                                                                                                              Claim
                                                                                                                                                                                      kidney, lung,
                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                           Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                  31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                               11-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9906548-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUN-1999
                            proliferation/differentiation activity, haematopoiesis regulating
                                                                                                                              AAX41094 to AAX41347 represent 5' expressed
                                                                                                                                                                                                                                                                                                                      (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
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                                                                                                                                                                                                                                                1999-153778/13.
DB; AAX41145.
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                                                                                                                                                            27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         secreted protein;
tissue growth regulating activity, reproductive
g activity, chemotactic/ chemokinetic activity, l
                                                                                                                                                           Page 682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132
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                                                                                                                                                                                                                                                                                            Dumas Milne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anti-inflammatory; tumour inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                     97US-0905135
                                                                                                                                                                                                                                                                                                                                                                                  98WO-IB01222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                         824pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.2%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                            Edwards
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 126; DB 21;
Pred. No. 1.2e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence
                                                                                                                sequence tags (ESTs) for
teins given in AAY12261 to
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signal per
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosis;
                                                                                                                                                                                                      prostate,
haemostatic
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RESULT 13
AAY64672
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Best Local S
Matches 116
         sequences, corresponding to human secreted proteins. AAY6451 to AAY6438 represent the EST-related proteins corresponding to AAZ4265 AAZ43052. The 5' ESTs can be used for producing secreted human gene products. They can be used to identify and isolate 5' untranslated regions (UTRs) and upstream regulatory regions which control the location, development stage, rate, and quantity of protein synthesis, well as stability of mRNA. The ESTs are also useful as probes for chromosome mapping, and to obtain full length cDNA clones. The ESTs calso be used in forensic procedures to identify individuals, or in diagnostic procedures to identify individuals having genetic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thrombolytic activity, receptor/ ligand activity, anti-inflammatory activity; tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a cell.
                                                                                                                                                                                                                                                                   WPI; 2000-038446/03
N-PSDB; AAZ42286.
                                                                                                                                                              AAZ42265 to AAZ43075 represent novel 5' expressed sequence
                                                                                                                                                                                                                         diagnostic,
                                                                                                                                                                                                                                      Novel
                                                                                                                                                                                                                                                                                                                                                                        09-APR-1998;
28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                   09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY64672 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy; chromosome mapping;
forensic; location; development;
                                                                                                                                                                                                                                                                                                                                                                                                                                               21-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9953051-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulation; identification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDK 147
                                                                                                                                                                                                                   secreted protein 5' expressed ostic, forensic, gene therapy,
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116; Conserv
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                                                                                                                                                                                         Page 604; 837pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 AA;
                                                                                                                                                                                                                                                                                                              Edwards
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; expressed sequence tag; secreted protein; diagnosis;
chromosome_mapping; upstream regulatory sequence;
                                                                                                                                                                                                                                                                                                                                                                        98US-0057719
98US-0069047
                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-IB00712.
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                                                                                                                                                                                                                                                                                                              Duclert
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Pred. No.
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protein synthesis; stability;
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                                                                                                                                                                                                                      sequence tag sequences used and chromosome mapping proce
                                                                                                                                                                                                                                                                                                            Giordano
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Best Local :
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13-APR-1998;
10-AUG-1998;
04-SEP-1998;
                                                                                                                   Extended specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy protocols. The nucleic acids encoding signal peptides can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell. The proteins encoded by the EST sequences may be useful in treating a variety of human conditions. Secreted proteins have therapeutic value, and the identification of new secreted proteins is valuable. ARX42249 to ARX42264 and ARX64644 to ARX6450 represent
                                                                                                                                                                                                                                                                                                                                                                                                       chromosome mapping; human; hereditary disease; diagnosis; cancer; hyperlipidaemia; cardiovascular; neurodegenerative disorder; therapy; autoimmune disease; rheumatic disease; embryogenic disorder; myopathy; renal injury; amino aciduria; hypoglycaemia; male rat infertility;
                                                                                                                                                        N-PSDB;
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                                                                                                                   cDNAs useful
antibodies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein; 131
                                                                                             Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 AA;
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98US-0081563.
98US-0096116.
98US-0099273.
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Pred. No.
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This sequence represents a human secreted protein of the invention. The extended cDNAs (or genomic DNAs obtainable from them) may be used to prepare PCR primers and probes. These are useful for forensic matching or positive identification by DNA sequencing. They may also be used in alternative fingerprint identification techniques. Antibodies against the proteins encoded by the extended cDNAs are useful in identification of

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therap; chromosome mapping; signal peptide; prostate; upstream regulatory sequence; cytokine activity, cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation and differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, chemotactic/chemokinetic activity, haemostatic ar
                                                                                                                                                        AAX40438 to AAX40715 represent 5' expressed sequence tags (ESTs) for human secreted proteins expressed in prostate, and encode the proteins given in AAX11716 to AAX11993 respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene
                                                                                                                                                                                                                                                                                                                                                                                                     New isolated prostate-derived nucleic acids - used to develop products which may have cytokine, immune regulatory, haematop regulating, anti-inflammatory or tumour inhibition activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9906550-A2
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                                                                                                                                                                                                                                                                                                                                               Claim 34; Page 603; 675pp; English.
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59; Conser
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6.9e-50;
thes 0;
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                                                                                                                               Sequence
            32 MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWT
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MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWT
                                                                               Similarity
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                                                              Conservative
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Pred. No.
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2.6e-46;
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Match Length
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JC5578
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
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3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4
484	478	473	465	455	449	408	408	404	402	396	390	386	381	369	352
N	2	N	N	2	N	N	N	1	2	N	N	N	1	2	2
T34016	S18158	S22621	B85358	T34412	AE1952	JC5674	PD0007	JC5150	JC5151	н82339	T22810	S53965	S15809	AG0386	S47006
hypothetical prote	lipoprotein Lipase	phosphomannomutase	SERINE CARBOXYPEPT	hypothetical prote	hypothetical prote	cytochrome P450 no	cytochrome P450 no	nitric-oxide reduc	nitric-oxide reduc	conserved hypothet	hypothetical prote	hypothetical prote	cytochrome P450 CY	5-amino-6-(5-phosp	zinc finger protei

## ALIGNMENTS

RESULT 1 JE0350

Biochem. Biophys. Res. Commun. 251, 111-116, 1998 A;Title: hAG-2, the human homologue of the Xenopus laevis A;Reference number: JE0350; MUID:99009231 A;Accession: JE0350

cement

gland gene XAG-2,

R; Thompson, D.A.; Weigel, R.J.

Anterior gradient-2 - human
C;Species: Homo sapiens (man)
C;Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 21-Jul-2000
C;Accession: JE0350

A;Cross-references: GB:AF007791; NID:g3779196; PIDN:AAC77358.1; PID:g3779197 C;Comment: This protein is coexpressed with estrogen receptor (ER) in breast

breast cancer

a

A;Gene: hAG-2 C; Genetics: A; Molecule type: mRNA A; Residues: 1-175 < THO>

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C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 26-Aug-1999
C;Accession: JC5201; Pc4303
R;Thomas, M.B.; Haines, S.L.; Akeson, R.A.
Gene 178, 1-5, 1996
A;Title: Chemoreceptors expressed in taste, olfactory and male reproductive A;Reference number: JC5200; MUID:97080538
A;Accession: JC5201
                                A; Molecule type: DNA
A; Residues: 1-315 <THO1>
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A; Cross-references: A; Accession: PC4303
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                                                                A; Status: preliminary; nucleic acid
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                GB:U50948; NID:g1256390; PIDN:AAC52910.1; PID:g1256391
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100.0%;
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; Pred. No. 9.4e-168;
                                                                  sequence
                                                                                                                      olfactory and male reproductive tissues
                                                                  not shown
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A;Status: preliminary
A;Molecule type: protein
A;Residues: 144-151;70-277 <THO2>
A;Residues: 144-151;70-277 <THO2>
A;Experimental source: taste bud
C;Comment: This protein is coupled to
C;Genetics:
A;Gene: tb567
C;Superfamily: olfactory receptor OR1
C;Superfamily: olfactory receptor OR1
C;Keywords: olfaction; taste bud; tra
F;26-49/Domain: transmembrane #status
F;101-120/Domain: transmembrane #status
F;101-120/Domain: transmembrane #status
F;101-120/Domain: transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable acyl-CoA dehydrogenase - Deinococcus radiodurans (strain C;SpecLes: Deinococcus radiodurans C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31 C;Accession: C75578
J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson M; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback S.; Smlth, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Genome sequence of A;Reference number: A75250; A;Accession: C75578 A;Status: preliminary
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Best Local Similarity
Thes 8; Conserv
                                                                           A; Reference number: A72450; A; Accession: C72486
                                                                                                                                 DNA Res. 6, 83-101, 1999
                                                                                                                                                      R; Kawarabayasi, Y.; Hino, Y.; awa, H.; Takamiya, M.; Masuda
                                                                                                                                                                                                                                                                                                                                                         ₽
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A; Residues: 1-637 <WHI>
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                                                                                                                 A; Title: Complete genome sequence
                                                                                                                                                                                                                                                     hypothetical protein APE2531 - Aeropyrum pernix (strain Kl)
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                                                                                                                                                                                              ;Species: Aeropyrum pernix;Date: 20-Aug-1999 #sequence_revision;Accession: C72486
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: GB:AE001863;
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                                    Molecule type: DNA
                                                        Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene: DRA0250
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  references:
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                      1-101 <KAW>
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8; Conser
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  DDBJ:AP000064;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the radioresistant bacterium Deinococcus radiodurans R1. {\tt MUID:20036896}
                                                                                               yuence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
MUID:99310339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .0%;
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, S.; Funahashi,
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NID:g5105945; PIDN:BAA81547.1;
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s predicted <TM6>
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                                                                                                                                                        H.; Yamazaki,
hashi, T.; Tan
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12;
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Tanaka, T.; Kudoh, Y.;
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, L.; Utterback, T.; Zalewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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C.; Ma
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  RESULT
B95024
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C;Superfamily: colipase
C;Keywords: lipid digestion; lipid hydrolysis; pancreas
C;Keywords: lipid digestion; lipid hydrolysis; pancreas
E;117/Domain: signal sequence #status predicted <SIG>
E;18-22/Domain: amino-terminal propeptide #status predicted <APP>
E;23-108/Product: colipase #status experimental <AAT>
E;23-108/Product: carboxyl-terminal propeptide #status predicted <CPP>
E;109-112/Domain: carboxyl-terminal propeptide #status predicted
E;34-104,40-56,44-80,45-78,66-86/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GDB:127277; OMIM:120105
A;Map position: 6pter-6p21.1
A;Introns: 28/3; 69/3
                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 23-108 <STE>
C;Comment: Colipase, a cofactor of triacylglycerol lipase
se the enzyme is washed off by bile salts, which are known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross references: GB:J02883; NID:g180885; PIDN:AAA52054.1; PID:g180886
A;Note: evidence of partial N-glycosylation, possibly at Asn-43
R;Sternby, B.; Engstrom, A.; Hellman, U.; Vihert, A.M.; Sternby, N.H.; Bc
Blochim. Biophys. Acta 784, 75-80, 1984
Biochim. Biophys. Acta 784, 75-80, 1984
A;Title: The primary sequence of human pancreatic colipase.
A;Reference number: A90652; MUID:84104937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:M95529; NID:g180842; PIDN:AAB05818.1; PID:g1483624 A;NOte: sequence extracted from NCBI backbone (NCBIN:110576, NCBIN:110578, R;Lowe, M.E.; Rosenblum, J.L.; McEwen, P.; Strauss, A.W. Biochemistry 29, 823-828, 1990
A;Title: Cloning and characterization of the human colipase cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: A42568; A33949; A03163
R;Sims, H.F.; Lowe, M.E.
Biochemistry 31, 7120-7125, 1992
A;Title: The human colipase gene: isolation, chromosomal location, A;Reference number: A42568; MUID:92353041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 19-May-1995 #text_change 08-Dec-2000
C:Accession: A42568; A33949; A03163
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C; Superfamily:
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A; Residues: 1-112 <LOW>
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밁
                                                                                                                                                                        F;69,72,75,76/Binding site: micellar substrate
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A; Residues: 1-112 <SIM>
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gasawara, N.; Yasunaga, T.; I
DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequ
A; Reference number: A99629; N
A; Accession: E90903
A; Status: preliminary
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D90784
                                                                                                                 hypothetical protein ECs2197 (imported) c;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision :C;Accession: E90903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gasawara, N.; Yasunaga, T.; Kuhara
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence
A;Reference number: A99629; MUID:2
A;Accession: D90784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein ECs1244 [imported] C:Species: Escherichia coli C:Date: 18-Jul-2001 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conserved domain protein SP0207 [imported] - Streptococcus pneumoniae (strain C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: B95024
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Petersor
                                                                 R;Hayashi, T.; Makino, K.; Ohnishi, gasawara, N.; Yasunaga, T.; Kuhara, DNA Res. 8, 11-22, 2001
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A; Residues: 1-114 <HAY>
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A; Residues: 1-112 < KUR>
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A;Accession: B95024
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N.; Yasunaga, T.; Kuhara,
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Escherichia coli
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MUID:21156231; PMID:11258796
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                                                                                Kurokawa, K.;
Shiba, T.; Hat
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Shiba, T.; Hattori,
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28;
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ttori, M.;
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M.R.;
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Radune,
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Shinagawa, H.
                                                                                  Yokoyama, K.;
Shinagawa, H.
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e, D.; Holtzapple,
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A; Cross-references: GB:BK
A; Cross-references: st:C; Genetics:
A; Gene: ECs2197
C; Superfamily: hypothetic
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C;Super1
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C; Superfamily: hypothetical protein b3024
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A;Residues: 1-14 <STO>
A;Cross-references: GB:AE005174; NID:g12515051; E
A;Experimental source: strain 0157:H7, substrain
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R;Perna, N.T.; Plunkett III, G.; Burland, V.;
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, &
Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                             unknown protein encoded within prophage CP-9330 [imported] - Escherichia ccC;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-200
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R;Perna, N.T.; Plunkett III, G.; Burland, V.;
iller, L., Grotbeck, E.J.; Davis, N.W.; Lim, I
Nature 409, 529-533, 2001
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A; Residues: 1-114 <STO>
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KALKLLK 203
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Pred. No.
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                                Pred. No. 28;
Mismatches
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28;
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28;
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A.; Dimalanta,
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                                                                                                                                                PIDN:AAG56169.1;
n EDL933
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lanta, E.;
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                                                                                                                                                                                                                                                                                                              J.D.; Rose,
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Potamousis,
                                                                                                                                                               GSPDB:GN00145;
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                                0;
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(strain

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UWGP:

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C:Species: Hydra magnipapillata (;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 01-Dec-2000 C;Accession: B41132; S21930 R;Kurz, E.M.; Holstein, T.W.; Petri, B.M.; Engel, J.; David, C.N. J. Cell Biol. 115, 1159-1169, 1991
                                                                                                                                             RESULT 13
B41132
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C; Superf
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A; Residues: 1-126 <KUR>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, i
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
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F90432
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A;Residues: 1-115 <STO>
A;Cross-references: GB:AE004537; GB:AE004091; NID:g9946960; PIDN:AAG04448.1; GSPDB:GN00.
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas A;Reference number: A82950; MUID:20437337
A;Accession: H83514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: H83514
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein PA1059 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa (C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 15-Feb-2002
                  A; Title: Mini-collagens
                                                                                                                       collagen-related protein 2 - Hydra magnipapillata (fragment)
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A; Accession: F90432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Description: Sulfolobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein SSO2594 [imported] - C; Species: Sulfolobus solfataricus
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Best Local :
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nes 7; Conser
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7; Conserve
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 jens in hydra nematocytes
A41132; MUID:92064646
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0; Mismatches
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K.R.; Kas,
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Larbig,
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K.; Lim,
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Query Match
Best Local Similarity
7; Conserve
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A; Residues: 1-205 <KI
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Best Local S
Matches 7
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                                                                                      spr0186
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                    Conservative
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R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S. e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S. y, P.; Sun, P.M.; Winkler, M.E. J. Bacteriol. 183, 5709-5717, 2001
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S. A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: B97895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Thems 7; Conserve
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R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved hypothetical protein STY1322 [imported] - Salmonella enterica subsp. enteric; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C;Accession: AH0652
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A;Status: preliminary
A;Nolecule type: mRNA
A;Residues: 1-142 <KUR>
A;Cross-references: EMBL:X61046; NID:g9448; PIDN:CAA43380.1; PID:g9449
A;Note: submitted to the EMBL Data Library, July 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein spr0186 [imported] - Streptococcus pneumoniae (strain C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A;Title: Complete genome sequence of a multiple drug resistant A;Reference number: ABO502; PMID:11677608
A;Accession: AH0652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001
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A; Residues: 1-167 <PAR>
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100.0%; Fitive 0;
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                                                                                                                                        PIDN: AAK98990.1;
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         DB
46;
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                                                                                                                                          GSPDB:GN00174
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use by non-profit institutions as lone
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                                                                                                                                                                                                                          "Interfacial activation of the lipase-procolipase conmicelles revealed by X-ray crystallography.";
Nature 362:814-820(1993).
-I- FUNCTION: COLIPASE IS A COFACTOR OF PANCREATIC LITTE LIPASE TO ANCHOR ITSELF TO THE LIPID-WATER IT COLIPASE THE ENZYME IS WASHED OFF BY BILE SALTS,
INHIBITORY EFFECT ON THE LIPASE.
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"The primary sequence of human pancreatic "The primary sequence of Auman pancreatic Acta 784:75-80(1984).
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Sternhy n -
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"The human collpase gene: isolation,
tissue-specific expression.";
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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MEDLINE-93241293; PubMed-8479519;
van Tilbeurgh H., Egloff M.-P., N
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Biochemistry 31:7120-7125(1992).
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MEDLINE=92353041; PubMed=1643046;
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Sive H., Bradley L.;
"A sticky problem: the Xenopus cement anteroposterior patterning.";
Dev. Dyn. 205:265-280(1996)
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PROSITE; PS00121; COLIPASE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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     DB
13;
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                   1;
                                                                                                                                                                                                                                                                                      Pipoidea;
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                                                                                                           Usage
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 0
                  Length 183;
                                    PROTEIN
8 CRC64;
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 Indels
                                                                                                                                                                           CEMENT
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                                                                                                                                                                                                                                                                                      Pipidae;
                                                                                                             and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                 POTTE HYACE STANDARD; PRT; 235 AA.

PO1513;

PO1-17UL-1986 (Rel. 01, Created)

PO1-JUN-1994 (Rel. 29, Last sequence update)

PO1-MAR-2002 (Rel. 41, Last annotation update)

Attacin E and F precursor (Immune protein P5).

S Hyalophora cecropia (Cecropia moth).

E Hyalophora ketazoa; Arthropoda; Tracheata; Hexapoda; In:

C Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossai

C Pterygota; Saturniidae; Saturniinae; Hyalophora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _XENLA
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P55869;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by ancomplete the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aberger F., Schueren C., Lepperdinger G., Richter K., Gr
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Secreted (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Cement gland;
                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=91160561; PubMed=2001705;
Sun S.C., Lindstroem I., Lee J.-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
  SEQUENCE OF
                                                                      cecropia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997
                                                                           "Structure and cecropia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kenopodinae; Kenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L5-JUL-1998 (Rel.
L5-JUL-1998 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 DPSLTVR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
SIMILARITY: HIGH, TO XENOPUS XAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVEL IN CEMENT GLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPSLTVR 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U82110;
                                             Biochem. 196:247-254(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 AA;
  48-235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB49974.1;
                                                                                             expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18
185
-- 20442 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35, Created)
36, Last sequence update)
36, Last annotation update)
protein NP77 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.4%;
100.0%;
                                                                                           Lee J.-Y.,
of the at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 7; DB 1; Pred. No. 13; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.

PUTATIVE SECRETED PROTEIN NP77.

AE3807C926044509 CRC64;
                                                                                           Y., Faye
attacin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                           I.;
genes
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                                                                                             in
                                                                                                                                                                                                                                                                  Glossata;
                                                                                             Hyalophora
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
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                                                                                                                                                                                                                                                                               RESULT
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Best Local
                                                                                                                                                                                                                               Matches
                                       UI-NOV-1997 (Rel. 35, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mast cell protease 1A precursor (EC 3.4.21.-)
Ovis ariss (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                         Insect in Repeat.
Repeat.
SIGNAL
PROPEP
                                                                                                                               SHEEP
                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                  CHAIN
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cecropia.";
EMBO J. 3:2065-2070(1984).
-!- FUNCTION: ATTACINS ARE
-!- PTM: ATTACIN F APPEARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boman H.G.;
"Insect immunity. Isolation
corresponding to acidic and
EMBO J. 3:2071-2075(1984).
                                Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- MISCELLANEOUS: THERE ARE SIX FORMS OF ATTACIN THAT ARE D INTO TWO GROUPS: ACIDIC (E AND F) AND BASIC (A, B, C, AN -!- SIMILARITY: BELONGS TO THE ATTACIN/SARCOTOXIN II FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Insect immunity. The primary attacin F and its relation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 48-235 FROM N.A.
MEDLINE-86005745; PubMed-3840100;
Boman H.G., Faye I., von Hofsten P., Kockum;
Xanthopoulos K.G., Bennich H., Engstroem A.,
                                                                                                       MCT1_SHEEP
P80931;
                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "On the primary structures of lysozyme, Hyalophora cecropia.";
                     Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Engstroem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 48-231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [4]
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                                                                                                                                              σ
                                                                                                                                                                                                       40 FLLLVAL
                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTACIN E
                                                                                                                                                                               FLLLVAL
                                                                                                                                                                                                                                                                                                                                                                                          S14104; S14104.
                                                                                                                                                                                                                                                                                                                                                                                                     A01775; EWWKEC.
                                                                                                                                                                                                                                                                                                                                                                                                                             X57715; CAA40886.1; -. X00869; CAA25414.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                 M34926;
                                                                                                                                                                                                                                                                                                                                                                             immunity;
                                                                                                                                                                                                                                         Similarity
                     Eutheria; Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunol.
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170
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                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                              Antibiotic;
                                                                                                                                                                                                                                                                                         19
47
235
231
169
235
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                                                                                                                                                                                                                                         3.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEMOLYMPH ANTIBACTERIAL PROTEINS.
TO BE DERIVED BY PROTEOLYTIC DIGESTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and se
                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                         ATTACIN E.
ATTACIN F.
GLY-RICH (G1).
GLY-RICH (G2).
                                                                                                                                                                                                                                         Score 7; |
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                             Hemolymph;
                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ao Z.-J., Carlsson A., structure of the anti two native attacins f
                                                                                                                                                                                                                                                                              35E1B549FB0417D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P., Lee J.-Y., Xanthopoulos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence of two cDNA clones
                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          attacins from Hyalophora cecropia.";
                      Ruminantia;
                                                                                                                                                                                                                                   DB 16;
                                                                                                                     245
                                                                                                                                                                                                                                                                                                                                                                             Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cecropins and attacins from
                                                                                                                     ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K., Lee J.-Y.,
, Merrifield R.B.,
                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                      Length 235;
                                                          (SMCP-1A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibacterial protein
                     Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from
                                                                                                                                                                                                                                                                                                                                                                             family; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bennich H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hyalophora
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Best Local S
Matches 7
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InterPro: IPR001254; Trypsin.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00772; CHYMOTRXPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1
PROSITE; PS00134; TRYPSIN_HIS; 1
PROSITE; PS00135; TRYPSIN_SER; 1
                                                                                                      ACT_SITE
ACT_SITE
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pemberton A.D., Huntley J.F., Miller H.R.P.;
"Sheep mast cell proteinase-1: characterization class of dual-specific ruminant chymases.";
Biochem. J. 321:665-670(1997).
-i- FUNCTION: HAS A CHYMOTRYPSIN-LIKE AND TRYPSI
                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 20-44.
Miller H.R.P., Huntley J.F., Newlands G.F.J.;
(In) Caughey G.H. (eds.);
Mast cell proteases in immunology and biology, pp.203-235,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 176-185 TISSUE-mast cells; MEDLINE-98343972; PubMed-9677343;
                                                                                                                                                                                                                                                 Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y14654; CAA74984.1; HSSP; P04187; 2CP1.
                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Secretory granules.
-!- TISSUE SPECIFICITY: MUCOSTL MAST CELLS.
-!- SIMILARITY: BELLONGS TO PEPFIDASE FAMILY S1; ALSO KNOWN
TRYPSIN FAMILY. GRANZYME SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97184650; PubMed-9032451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             on substrate specificity."; Biochem. J. 333:801-809(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sheep mast-cell proteinases-1 and structure and molecular modelling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McAleese S.M., Pemberton Miller H.R.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Gastric mucosa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dekker, New York (1995).
                                                                                                                                                                                                                                                                                                                                                                     MEROPS; S01.142;
                          40
 4
               FLLLVAL
FLLLVAL
                                                    Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF 20-29
                                                                                                      245
                                                                                                                                                                                                                                                  Serine protease;
                                                                                                                                18
20
63
107
201
48
141
                                                     Conservative
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245
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107
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186
207
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                                                                100.0%;
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                                                                                                                POTENTIAL.

ACTIVATION PEPTIDE.

ACTIVATION PEPTIDE.

MAST CELL PROTEASE 1A.

CHARGE RELAY SYSTEM (BY S
BY SIMILARITY.
                                                               Score 7;
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RESULT 7 MCT3\_SHEEP

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RESULT 8
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Matches 7
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P76462;
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Mast cell protease 3 precursor (EC 3.4.21.-) (SMCP-3).
Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sheep mast-cell proteinases-1 and -3: cDN structure and molecular modelling of the e on substrate specificity.";
Biochem. J. 33:801-809(1998).
-!- FUNCTION: HAS A CHYMOTRYPSIN-LIKE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                          SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOW; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00089; trypsin;
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InterPro; IPRO01254; Trypsin.
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RESULT 9
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075897;
16-0CT-2001 (Rel. 4
16-0CT-2001 (Rel. 4
16-0CT-2001 (Rel. 4
                 gene clor
Genomics
                                                                   SEQUENCE FROM N.A.
MEDLINE-20247255; PubMed-10783263;
Freimuth R.R., Raftogianis R.B., Wood T.C.,
Siciliano M.J., Weinshilboum R.M.;
                                                                                                                                                            Sakakibara Y., Yanagisawa K., Katafuchi J., Ringer D. Nakayama T., Suiko M., Liu M.-C.; "Molecular cloning, expression, and characterization SULTIC sulfotransferases that catalyze the sulfonatic N-hydroxy-2-acetylaminofluorene."; J. Biol. Chem. 273:33929-33935(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., M. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-KIZ / MG1655;
STRAIN-KIZ / MG1655;
MEDLINE-97426617; PubMed-9278503;
MEDLINE-97426617; PubMedt G. III, Bloch C.
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                TISSUE=Fetal
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MEDLINE=99069375; PubMed=9852044;
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YFAP OR B2225
               "Human sulfotransferases SULTIC1 and SULTIC2: gene cloning, and chromosomal localization."; Genomics 65:157-165(2000).
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Matches 7
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01-FEB-1995
01-FEB-1995
01-MAR-2002
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Barrell B.G., Badcock K., Bankler A.T., Bowman S., Brown D.,
Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones
Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S.V., Whitehead S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                     CHARACTERIZATION.
MEDLINE-98301591;
Taura T., Krebber
                                                                                                                                                                                     CHARACTERIZATION. MEDLINE-98058988;
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EMBL; AF186263; AAF72810.1;
HSSP; P50224; 1CJM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00685;
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                                                                                                                         homologue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RANBP2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
                                                                                                        Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SULFATE CONJUGATION OF MANY DRUGS, XENOBIOTIC COMPOUNDS, AND NEUROTRANSMITTERS. MAY BE INVOLVED IN THE ACTIVATION CARCINOGENIC HYROXYLAMINES. SHOWS ACTIVITY TOWARDS P-NITT AND N-HYDROXY-2-ACETYLAMINO-FLUORENE (N-OH-2AAF).

SUBCELULAR LOCATION: Cytoplasmic.
SUBCELULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN FETAL LUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE SULFOTRANSFERASES FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                 FROM
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      of
                                                                                                                                                                3058988; PubMed=9395535; Schlenstedt G., Silver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302
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(Rel. 31,
(Rel. 41,
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Conservative
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C H., Silver P.A.; Ran-binding protein
                     PubMed=9636166;
H., Silver P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sulfotransfer;
                                                                                                        31877-31884(1997)
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35534 MW;
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cota; Saccharomycotina;
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Pred. No.
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    family, Yrb2p,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces
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RESULT 11
GCS1_YEAST
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Best Local S
Matches 7
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P35197;
01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                          Rasmussen S.W.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ
-1- FUNCTION: PLAYS A ROLE IN THE RESUMPTION O
-PROLIFERATION FROM STATIONARY PHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTPase activation; SEQUENCE 327 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nuclear protein export.";
                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeas Eukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1994
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc.
                                                                                                                                                                                                                        "A member of a novel family of yeast the transition from stationary phase EMBO J. 13:3812-3821(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                  Zinc finger protein GCS1 OR YDL226C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00160; RanBD;
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                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                     Ireland L.S., Johnston G.C., Drebot
Hoekstra M.F., Singer R.A.;
                                                                                                                                                                                                                                                                                                      MEDLINE=94349929; PubMed=8070409;
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00638; Ran_BP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000697; RanBP1_WASPInterPro; IPR000156; Ran_BP1.
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les 7; Conser
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                                                                                             SUBCELLULAR LOCATION: Nuclear (Probable).
SIMILARITY: BELONGS TO THE GCS1/GLO3/SPS18 FAMILY.
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S0001325; YRB2.
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non-profit institutions and this statement is not
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(Rel. 28, Last sequence up)
(Rel. 35, Last annotation)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Institute of Bioinformatics
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he export of protein conaining nuclear
f the nucleus. Stimulates the GTPase
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OF YEAST CELL
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RESULT 12
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                                                                                                                                                                                                  SMART; SM0010
Zinc-finger;
ZN_FING
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Horii M., Ishizaki T., Paik S.Y., Ma
"An operon containing the genes for
cytochrome p-450-like protein from a
J. Bacteriol. 172:3644-3653(1990).
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PRINTS; PR00405; REVINTRACTNG.
SMART; SM00105; ArfGap; 1.
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InterPro; IPR001164; Znf_GCS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M31939; AAA26718.1; -. HSSP; Q00441; 10XA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-90299781; PubMed-2361941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1931;
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   213 AFLLLVA 219
                                                                                                                                                      Local
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                                                            39 AFLLLVA
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26 49 C4-TYPE.
27 M -> I.
29 29 C -> Y (IN GC
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Streptomycineae; Str
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(EC 1.14.-.-).
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95096031; PubMed=7798191; Tomura D., Obika K., Fukamizu A., Shoun H.; Notice reductase cytochrome P-450 gene, CYP 55, of the fungus Fusarium oxysporum containing a potential binding-site for FNR, the transcription factor involved in the regulation of anaerobic growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YML107C OR YM8339.12. Saccharorror
                                                                                                                                                                                           "Nucleotide sequence of the unique nitrate/nitrite-inducible cytochrome P-450 cDNA from Fusarium oxysporum.";
J. Biol. Chem. 266:10632-10637(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomy Hypocreales; mitosporic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reductase) (P450 NOR).
CYP55A1 OR CYP55.
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND STRAIN-MT-811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusarium oxysporum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomycetales;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes.
                                                                                                                              SEQUENCE FROM
STRAIN=MT-811;
                                                                                                                                                                                                                                                                    Yasui T., Shoun H.;
                                                                                                                                                                                                                                                                                          Kizawa H.,
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                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=5507;
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386 AA; '
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D., Oda M., Fuk
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ascomycota;
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100.0%; Pr
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e EMBL/GenBank/DDBJ databases.
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Pred. No.
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reales; Fusarium
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EMBL; D14517; E
PIR; A40401; A4
PIR; JX0335; JX
PDB; 1ROM; 15-0
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Lee D.-S., Park S.-Y., Yamane K., Obayashi E., Hori "structural characterization of n-butyl-isocyanide c cytochromes P450nor and P450cam.";
Biochemistry 40:2669-2677(2001).
-!- FUNCTION: INVOLVED IN A DISSIMILATORY REDUCTION AS A NITRIC OXIDE REDUCTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR;
PDB;
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Nakahara K., Shoun H., Obayashi E., Nakamura H., Iizuka T.
"Crystal structure of nitric oxide reductase from denitrii
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J. Biochem. 116:88-94(1994).
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HSSP; P23295; 1F24.

InterPro; IPR001128; Cyt_P450.

Pfam; PF00067; p450; 1.

PRINTS; PR00359; BP450.

PROSITE; PS00086; CYTOCHROME_P450; FALSE_NEG.
PROSITE; PS00086; CYTOCHROME_P450; FALSE_NEG.
PROSITE; MONOOXYGENASE; HEME.

OX1doreductase; Monooxygenase; HEME (BY SIMILARITY BINDING 352 352 HEME (BY SIMILARITY BINDING 403 AA; 44273 MW; 1C2AB643FD219534
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STRAIN-1FO 30561;
MEDLINE-97163854; PubMed-9010609;
Kudo T., Tomura D., Liu D.L., Dai X.Q., Shoun H.;
"Two isozymes of P450nor of Cylindrocarpon tonkinense: molecular cloning of the cDNAs and genes, expressions in the yeast, and the putative NAD(P)H-binding site.";
BIOCHIMIE 78:792-799(1996).

-I- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Cytochrome P450 55A2 (EC 1.14...) (Cytochrome P450NOR1).
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Hypocreales; Nectriaceae; Neonectria.
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091er9 cydia pomon
047957 phoxinus eo
056157 streptomyce
09y8v3 aeropyrum p
09gzt3 homo sapien
Q97sv7 streptococc
Q9kxa4 escherichia
Q9xjm3 bacteriopha
                                                                                                                                                                                                                                                                                                                                          Description
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Q9sj37 arabidopsis	Q9SJ37	10	318	3.4	7	15
musca	Q9NGT1	ۍ	308	3.4	7	4
Q96hp9 homo sapien	Q96HP9	4	304	3.4	7	3
	Q9Z248	11	303	3.4	7	12
Q9plm7 chlamydia m	Q9PLM7	16	301	3.4	7	11
Q9wrt4 macaca mula	Q9WRT4	12	299	3.4	7	0
	Q9KZI2	2	299	3.4	7	39
Q51756 pseudomonas	Q51756	2	296	3.4	7	38
5	Q96BG3	4	295	3.4	7	37
	Q9IUA3	15	291	3.4	7	36
Q9skil arabidopsis	Q9SKI1	10	277	3.4	7	35
	P91894	u	276	3.4	7	34
	Q02304	Ν	272	3.4	7	33
Д	Q95KW7	6	269	3.4	7	32
	027451	17	261	3.4	7	31
Q9j218 macaca mula	Q9J2L8	12	257	3.4	7	30
Q9fj08 arabidopsis	Q9FJ08	10	257	3.4	7	29
	Q9EWR7	2	227	3.4	7	28
Q95xx7 caenorhabdi	Q95xx7	ر.	188	3.4	7	27
l xenopus	042251	13	185	3.4	7	26
	Q951I9	æ	173	3.4	7	25
o	Q951J1	œ	173	3.4	7	24
Q96za8 sulfolobus	Q96ZA8	17	169	3.4	7	23
	Q9V6R3	ഗ	167	3.4	7	22
	Q9L435	Ν	167	3.4	7	21
5	Q00485	ഗ	142	3.4	7	20
7	Q97VM7	17	126	3.4	7	19
715 s	Q05715	w	120	3.4	7	8
Q9i4r5 pseudomonas	Q9I4R5	16	115	3.4	7	17

## ALIGNMENTS

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ADD DE RELEGIOR DE RELEGIO DE REL
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              Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF038451; AAC82614.1; -.
EMBL; AF007791; AAC77358.1; -.
EMBL; AF008867; AAF22484.1; -.
EMBL; BC015503; AAH15503.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           095994 PRELIMINARY; PRT; 175 AA.
095994;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SECRETED CEMENT GLAND PROTEIN XAG-2 HOMOLOG (ANTERIOR GRADIENT (XENERUS LAEVIS) HOMOLOG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Zhang J.S., Smith D.I.;
Thuman homolog of XAG is differentially expressed in tumors.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thompson D.A., Weigel R.J.; "hAG-2, the human homologue of the Xenopus laevis cement gland gen XAG-2, is coexpressed with estrogen receptor in breast cancer cell
    SEQUENCE
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=COLON ADENOCARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 251:111-116(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99009231; PubMed=9790916;
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    ¥;
F271B1BD377BEE11 CRC64;
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Length 175;

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RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Saito R.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kachi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincish S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincish S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RT "Functional Salawa Salaw
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Best Local
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01-NOV-1998 (TrEMBLrel. 08, Last
01-DEC-2001 (TrEMBLrel. 19, Last
GOB-4 PROTEIN (ANTERIOR GRADIENT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thompson D.A., Weigel R.J.; "hAG-2, the human homologue of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-BALB/C; TIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    088312;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XAG-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
                                         Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. Biophys. Res. Commun. 251:111-116(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99009231;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning of a gene, gob-4, which is expressed cells in mice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Komiya
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Hirohashi S.;
                                                          annotation
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100.0%; Pred. No. 2.4e-173;
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                                                          full-length mouse
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2) (XENEPUS LAEVIS) (XENOPUS
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EMBL; BC013334; AAH13334.1; -...
MGD; MGI:1344405; AG72.
SEQUENCE: 175 AA.
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Submitted (ANG-2001) to the El
EMBL; AB016592; BAA32044.1; -
EMBL; AF044262; AAC72705.1; -
EMBL; AK007677; BAB25181.1; -
EMBL; BC013334; AAH13334.1; -
                                                                                                                                                                                             MLR6569 PROTEIN.
MLR6569.
Rhizobium loti (Mesorhizobium loti).
Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision;
Bacteria; Proteobacteria; besorhizobium.
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Q90Y05;
01-DEC-2001
01-DEC-2001
01-DEC-2001
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Q988W1;
01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       laevis embryo.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ EMBL; AF314056; AAL26844.1; -. 730n633041888
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasam Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto Takeuchi C., Yamada M., Tabata S.;

"Complete genome structure of the nitrogen-fixing symbiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CEMENT GLAND-SPECIFIC PROTEIN CGS.
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                             STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                        SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                     01-OCT-2001
01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Three novel genes expressed
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Alexandrova E.M., Novoselov V.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8355;
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MEDLINE=20036896; PubMed=10567266; White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson White O., Elsen J.A., Gwinn M.L., Nelson W.C., Richardson Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
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MEDLINE-97080538; PubMed-8921883;
Thomas M.B., Haines S.L., Akeson
"Chemoreceptors expressed in tast
tissues.";
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Bacteria; Thermus/Deinococcus
NCBI_TaxID=1299;
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-CCT-2001 (TrEMBLrel. 18, Last ann
ACYL-COA DEHYDROGENASE, PUTATIVE.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-NOV-1996 (TIEMBLIEL. 01, Last sequence update)
01-DEC-2001 (TIEMBLIEL. 19, Last annotation update)
TASTE BUD RECEPTOR PROTEIN TB 567.
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DNA Res. 7:331-338(2000).
EMBL; AP003009; BAB52836.1;
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EMBL; U50948; AAC5
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PF00001; 7tm_1; 1.

TE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

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   chardson D.L.,
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Zalewski C.,
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STRAINEY, CN BW SP;
STRAINEY, CN BW SP;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlsor Stapleton M., Brokstein P., Hong L., Agbayani A., Carlsor Champe M., Chavez C., Dorsett V., Farfan D., Frise E., Ge Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Munga Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY051898; AAK93322.1;
EMBL; AY051898; AAK93322.1;
SEQUENCE 1232 AA; 136912 MW; CEF6003D6939A6DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata;

Pterygota; Neoptera; Endopterygota; Diptera

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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Pfam; PF00441; Acyl-CoA_dh; 2
Pfam; PF02770; Acyl-CoA_dh_M;
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Science 286:1571-1577(1999).
EMBL; AE001863; AAF12388.1;
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RA Ballew R.M., Hasu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Bellew R.M., Hasu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.J., Evanley S., Dahlke C., Davenport L.B., Davies P.,
RA Clodek A., Goup L., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gann P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gann P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gann P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Karvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Marvey D., Helman T.J., Kennison J.A., Ketchum K.A.,
RA Glodek A., Gong F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Harris N.L., Marvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N., Wallson K.A., Nixon K., Nusskern D.R., Welberson D.L.,
RA Melson D.R., Welson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Welson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Mang Z.-Y., Wassarman D.A., Welnson M., Skupski M.P., Santh T.,
RA Wang Z.-Y., Wassarman D.A., Welnson M., Skupski M.P., Santh T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98418511; PubMed-9747739; Kang W., Tristem M., Maeda S., Crook N.E., O'Reilly D.R.; "Identification and characterization of the Cydia pomonel granulovirus cathepsin and chitinase genes."; J. Gen. Virol. 79:2283-2292(1998).
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         NADH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kang W., Crook N.E., Winstanley D., O'Reilly D.R.; "Complete sequence and transposon mutagenesis of the BamHI J fragment of Cydia pomonella granulosis virus."; Virus Genes 14:131-136(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-MEXICAN 1;
MEDLINE-97380577; PubMed-9237352;
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iEC-2001 (TremBLrel. 19, Last annotation update)
DEHYDROGENASE SUBUNIT 6 (FRACMENTY)
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NCE 73 AA; 8302 MW;
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5. 26;
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Q1-NOV-1996 (TrEMBLrel. 01, Create
01-JAN-1999 (TrEMBLrel. 09, Last s
01-DEC-2001 (TrEMBLrel. 19, Last a
C-5 ANTHRONE OXIDASE (FRAGMENT)
Streptomyces venezuelae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yang K., Han L., Ayer S.W., Vining L.C.
"Accumulation of the angucycline antibi
disruption of an oxygenase gene in the
cluster of Streptomyces venezuelae.";
Microbiology 142:0-0(0).
                                                                                                       Submitted (DEC-1998) to the EMBI EMBL; U28382; AAC98518.1; -. InterPro; IPR001064; Crystallin.
                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-SP5230;
                                                                                                                                                                                                                                                                                                                                                      Yang K.;
Submitted (JUN-1995)
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ACEI_TaxID=54571;
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MEDLINE=96146057; PubMed=8581159;
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Mol. Ecol. 4:745-753(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-96137174; PubMed-8564012;
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01-MAR-2001
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                                                                                                                                                          SEQUENCE FROM N.A. Xu X., Yang Y., Gao G., Xiao Xu X., Yang Y., Gao G., Xiao Submitted (MAY-2000) to the EMBL; AF271779; AAG44790.1; EMBL; AF253980; AAG44629.1;
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Ko Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; "Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999
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01 AA; 10277 MW; B8AF0E9B098E25B3 CRC64;
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CONSERVED DOMAIN PROTEIN.
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Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
"Complete genome sequence of a virulent isolate of Streptococcus
pneumoniae.";
                                                                                                                                                                                                                                                                                                                                                                                                                      O9KXAA;
O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 12.4 KDA PROTEIN.
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Science 293:498-506(2001).
EMBL; AE007335; AAK74387.1; -.
TIGR; SP0207; -.
"Complete nucleotide sequence of the prophage VT2-Sakai carrying the verotoxin 2 genes of the enterohemorrhagic Escherichia coli 0157:H7 derived from the Sakai outbreak.";
                                                                           MEDLINE=20198780; PubMed=10734605; Yutsudo C.H., Makino K., Yokoyama K., Kubota Y., Yutsudo C.H., Kurokawa K., Ishii K., Hattori M., Tatsuno I., Ak Yamamoto K., Ohnishi M., Hayashi T., Yasunaga T., Sasakawa C., Shinagawa H.;
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EMBL; AP000422; BAA94180.1; -.
                                     197 KALKILK 203
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114 AA; 1:
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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US-08-916-576B-7
US-08-916-576B-7
US-08-916-576B-7
US-08-913-359-28
US-08-471-496-9
US-08-471-496-9
US-08-471-496-2
US-08-63-552-1
PCT-US93-05704-1
US-08-063-552-1
PCT-US93-05704-1
US-08-063-552-2
US-08-063-552-3
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US-08-063-552-3
US-08-063-552-3
US-08-044-133-13
US-08-944-133-13
US-08-194-981E-42
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                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Appli
Sequence 106, App
Sequence 174, App
Sequence 6, Appli
                           sequence 6, Appli
sequence 7, Appli
sequence 10, Appl
sequence 11, Appli
sequence 11, Appli
sequence 28, Appli
sequence 9, Appli
sequence 9, Appli
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ALIGNMENTS	6	6	6	6	σ	6	σ	σ	σ	σ	6	σ	6	6	0	σ	6	6
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	118	118	117	116	116	116	110	92	92	76	76	76	63	55	44	44	44	29
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		US-08-545-809A-116	US-08-545-809A-114	US-08-545-809A-140	US-08-545-809A-118	US-08-545-809A-92	US-08-858-207A-273	US-09-309-487-22	US-09-309-487-21	US-09-309-487-29	US-09-309-487-16	US-09-309-487-14	US-09-326-039-2	US-09-227-357-216	US-08-714-524D-31	US-08-484-101B-31	US-08-530-010-31	US-08-194-981E-44
	123				Sequence 118, App		۳.			Sequence 29, Appl		•	Sequence 2, Appli	Sequence 216, App	`	Sequence 31, Appl	•	Sequence 44, Appl

## RESULT 1 US-08-916-576B-2 US-08-916-576B-2 ; Sequence 2, Application US/08916576B ; Patent No. 6171816 Query Match Best Local Similarity Matches 175; Conserv TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: GENERAL INFORMATION: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/916,576B FILING DATE: FILING DATE: APPLICANT: NAME: STEFFE, ERIC K. REGISTRATION NUMBER: 36,688 REFERENCE/DOCKET NUMBER: 141 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 371-2600 CLASSIFICATION: 536 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/024,347 FILLING DATE: 23-AUG-1996 ATTORNEY/AGENT INFORMATION: ANTORNEY/AGENT INFORMATION: APPLICANT: EBNER, REINHARD APPLICANT: ENURESS, GREGORY A. TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS MOLECULE TYPE: protein CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: ADDRESSEE: STERNE STREET: 1100 NEW CITY: WASHINGTON STATE: DC LENGTH: TYPE: a COUNTRY: ZIP: 200 TOPOLOGY: amino acid )GY: linear RY: US 20005-3934 175 amino acids E: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C. 1100 NEW YORK AVENUE, SUITE 600 YU, GUO-LIANG DILLON, PATRICK J. EBNER, REINHARD 85.0%; 45 2: 1488.0500001 Score 175; DB 4; L, Pred. No. 1.3e-159; 0; Mismatches 0; Length 175;

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32 MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE 91

Conservative

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CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER APPLICATION NUMBER: 60/099,273
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SOFTWARE: Patent.pm
SEQ ID NO 106
LENGTH: 175
                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                               Sequence 174, Application US/09247155A Patent No. 6312922
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Best Local :
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                                 APPLICANT: Dumas Milne Edwards, Jean-Baptiste APPLICANT: Duclert, Aymeric APPLICANT: Bougueleret, Lydie TITLE OF INVENTION: Complementary DNAS FILE REFERENCE: GENSET.021A CURRENT APPLICATION NUMBER: US/09/247,155A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Complementary DNAs FILE REFERENCE: GENSET.021A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dumas Milne Edwards, Jean-Baptiste APPLICANT: Duclert, Aymeric
EARLIER APPLICATION NUMBER: 60/074,121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bougueleret, Lydie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SIGNAL LOCATION: -20..-1
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                                                                                                                                                                                                                                                                                                       121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 85.0%; Score 175; DB 4; Local Similarity 100.0%; Pred. No. 1.3e-159; nes 175; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                          61 ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP 120
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10. 631291
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TOPOLOGY:
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US-08-916-576B-6
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EARLIER APPLICATION NUMBER: 60/081,563
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
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Best Local Similarity
Matches 59; Conserv
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SEQ ID NO 174
LENGTH: 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: SIGNAL NAME/KEY: SIGNAL LOCATION: -20..-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                         TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                              CLASSIFICATION: 536
PRIOR APPLICATION UNMBER: US 60/
APPLICATION NUMBER: US 60/
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: UNSURE LOCATION: 40,41,43,60,70,76,82,86,105,107
OTHER INFORMATION: Xaa = any one of the twenty amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,576B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: YU, GUO-LIANG
APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
               SEQUENCE CHARACTERISTICS LENGTH: 166 amino aci
                                                                                                    REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
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amino acid
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               166 amino acids
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100.0%; pr
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Pred. No.
                                                                                                                                                  1488.0500001
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E, SUITE 600
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5.6e-49;
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DILLON, PATRICK J.

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RESULT 6
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US-08-916-576B-8
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Sequence 7, Application US/08916576B Patent No. 6171816
GENERAL INFORMATION:
APPLICANT: YU, GUO-LIANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: YU, GUO-LIANG
APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 140
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/024,347
FILING DATE: 23-AUG-1996
ATTORNEY_AGENT INFORMATION:
NAME: STEFFE_ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                       170 amino acids
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100.0%; Pred. No.
tive 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KESSLER, GOLDSTEIN & FOX, P.L.L.C. ORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/916,576B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
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Pred. No.
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                                                                                                                                                                          Mismatches
                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                      1.9e-15;
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                                                                                                                                                                                                    Length 170;
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RESULT 7
US-08-063-552-10
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                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/08063552 Patent No. 5688936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6
FILING DATE: 23-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                          APPLICANT: Edwards, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 23-AUG-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                               140 DPSLTVR 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 DPSLTVR 169
                                                                                                                                                                                           STREET: 225 SOU
CITY: Pasadena
                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
mes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
CLASSIFICATION:
             APPLICATION NUMBER: UFILING DATE: 19930514
                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: STEFFE, ERIC K. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                              91101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                            California
                                                                                                                                                                                                            225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C. 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                              USA
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JENTION: NOVEL HUMAN GROWTH FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                            Sheldon & Mak
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100.0%;
                                                                                                                                                                                                                                                                            Vesicle Membrane Transport Proteins
                                                                                                                                                                                                                                                                                             Robert H
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                           US/08/063,552
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Pred. No
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ATTORNEY/AGENT INFORMATION:

Farber, Michael

REGISTRATION NUMBER:

32,612

9067-1

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Query Match
Best Local Similarity
"hes 7; Conserve
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GENERAL INFORMATION:
APPLICANT: Edwards, Robert H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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HYPOTHETICAL: NO
FRAGMENT TYPE: J
ORIGINAL SOURCE:
ORGANISM: RAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (818) 795-6321 INFORMATION FOR SEQ ID NO: 10:
                                                                                   TOPOLOGY: line
MOLECULE TYPE: P
HYPOTHETICAL: NC
FRAGMENT TYPE: 1
ORIGINAL SOURCE:
ORGANISM: Ratt
                                                                                                                                                                                                                             TELEFAX: (818) 795-6321 INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 220 amino acid
                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 220 amino acid
                                                                                                                                                                                                                                                          TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 ALLLDNM 195
                                                                                                                                                                                                                                                                                         NAME: Farber, Michael B
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9067-1PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 225 500
CITY: Pasadena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 ALLLDNM 26
                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PIFILING DATE: 19930611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100 es 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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AMINO ACID
DGY: linear
                                                                                                                                                                             AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                               220 amino acids
        3.4%; Score 7; DB 11arity 100.0%; Pred. No. 40 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                      Rattus rattus
                                                                                                                                                                    linear
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                                                                                                                     internal
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                                                                                                                                                peptide
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100.0%; Pr
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s; Pred. No. 40;
0; Mismatches
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                         DB 5;
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           0;
                                      Length 220;
           Indels
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         0;
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           Gaps
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GENERAL INFORMATION:
APPLICANT: Bach, Lisbeth
APPLICANT: Obmann, Anders
APPLICANT: Breinholt, Jens
APPLICANT: Fuglsang, Claus C.

APPLICANT:

RESULT 10 US-08-993-359-28

Sequence 28, Application US/08993359A Patent No. 6039942

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US-08-773-870-1
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                                                         Matches
                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: Herewith CLASSIFICATION: 435
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                          IMMEDIATE SOURCE:
LIBRARY: Consens
CLONE: Consensus
                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K
              164 PSLTVRA 170
132 PSLTVRA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 ALLLDNM
                                                 J. 48; Score 7; Local Similarity 100.0%; Pred. Notes 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 3174 POI
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 ALLLDNM
                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                      TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
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                                                                                                                                                                                                            LENGTH:
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                                                                                                                                           Consensus
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                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Incyte Pharmaceuticals, Inc.
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N: NOVEL HUMAN MAGE-LIKE PROTEIN
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                                                                                                                                                                                                                                                                                                               PF-0179 US
                                                         Mismatches
                                                                       No.
                                                                                   DB 2;
                                                                       69;
                                                                                   Length 411;
                                                         0; Indels
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                                                         Gaps
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OF INVENTION: Phytase Polypeptides REFERENCE: 5383.500-US

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; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-08-993-359-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.4%; Score 7; Best Local Similarity 100.0%; Pred. No. Matches 7; Conservative 0; Mismatc
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                                                                                                                     APPLICATION NUMBER: US/08/471,496
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US95/02645
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 1388/97
EARLIER FILING DATE: 1997-12-01
EARLIER APPLICATION NUMBER: 60/046,082
EARLIER FILING DATE: 1997-05-09
NUMBER OF SEQ ID NOS: 32
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CURRENT FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 1480/96
EARLIER FILING DATE: 1996-12-20
EARLIER APPLICATION NUMBER: 1481/96
EARLIER FILING DATE: 1996-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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EARLIER FILING DATE: 1997-03-18
EARLIER APPLICATION NUMBER: 0529/97
EARLIER FILING DATE: 1997-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0
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REFERENCE/DOCKET NUMBER: 14/
REFERENCE/DOCKET NUMBER: 14/
TELECOMMUNICATION INFORMATION:
TELEPAN: (202) 371-2600
TELEPAN: (202) 371-2540
NFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: ROSEN, CRAIG
TITLE OF INVENTION: HUMAN AMINE TRANSPORTER
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      383 RLSCAGT 389
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                                                                                                      1488.0830001
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US-08-894-840-9
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RESULT 13
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                                                                                                        Query Match
Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
Matches 7; Conserv
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APPLICANT: LI, YI
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TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 9:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/00
FILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CAO, LIANG
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: HUMAN AMINE TRANSPORTER
NUMBER OF SEQUENCES: 9
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                                                                            189 ALLLDNM 195
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TOPOLOGY: lir
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                                              30 ALLLDNM
                                                                                                                                                                                                                                     TYPE: amino acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ilarity 100.0%; Pred. No. 77
Conservative 0; Mismatches
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100.0%; Pred. No.
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5. 77;
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5. 77;
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US-09-139-675-9 ; Sequence 9, Application US/09139675A ; Patent No. 6117426

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GENERAL INFORMATION:

APPLICANT: Li, Yi

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TYPE: amino acid;
TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-471-496-2
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Best Local Similarity
Watches 7; Conserva
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APPLICANT: Rosen, Craig
APPLICANT: Rosen, Craig
TITLE OF INVENTION: Human Amine Transporter
FILE REFERENCE: 1488.0830003
CURRENT APPLICATION NUMBER: US/09/139,675A
CURRENT FILING DATE: 1998-08-25
EARLIER APPLICATION NUMBER: WO PCT/US95/02645
EARLIER APPLICATION NUMBER: WO PCT/US95/02645
EARLIER APPLICATION NUMBER: US 08/471,496
EARLIER FILING DATE: 1995-06-06
RUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Rattus sp. US-09-139-675-9
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US-08-471-496-2
                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,496
FILING DATE: 06-JUN-1995
CLASSIFICATION OBTA:
APPLICATION NUMBER: WO PCT/US95/02645
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0830001
TELECOMMUNICATION INFORMATION:
TELECHONE: (202) 371-2540
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SEQ ID NO 9
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: ROSEN, CRAIG
TITLE OF INVENTION: HUMAN AMINE TRANSPORTER
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                          TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 465
TYPE: PRT
                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 470 amino acid
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30 ALLLDNM 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, SUITE 600
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                                                                                                                                 470 amino acids
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3.4%;
100.0%;
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 Mismatches

  Score 7;
Pred. No.
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                    Length 470;
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                                                                                                                   Query Match
Best Local Similarity
The 7; Conserve
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Search completed: October 9, 2002, 16:45:11 Job time : 19 secs
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 470 amino acids
                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/894,840 FILING DATE: 29-AUG-1997 ATTORNEY/AGENT INFORMATION: NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: HUMAN AMINE TRANSPORTER
NUMBER OF SEQUENCES: 9
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                                                                                                   189 ALLLDNM 195
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                                                                   30 ALLLDNM 36
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ZIP: 20005-3934
                                                                                                                                                                                                                                                    TYPE:
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STREET: 1100 NEW YORK AVENUE, SUITE 600
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                                                                                                                                    3.4%; Score 7; DB 2;
100.0%; Pred. No. 78;
ive 0; Mismatches
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gb_pr:BC015503
gb_pat:AR123828
gb_pat:AX067336
gb_pat:AX341388
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gb_pat: Ax341524
gb_pat: Ax340668
gb_pat: Ax341139
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gb_pat:AR123857
gb_pat:AX340984
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gb_pat:AX341116
gb_pat:AR166839
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gb_ro:BC013334
gb_pat:AX192616
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gb_ro:AB016592
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gb_pat:AX341953
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gb_pr:AF007791
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gb_pat:AR177410
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gb_pat:AX341084
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gb_pat:AX015056
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Query length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Command line parameters:
                                        gb_pat:AX193063
gb_pat:AR123830
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gb_pat:AX341229
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Database length: 1873333701
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DEFINITION Sequence 8 from Patent W09955858.
ACCESSION AX011612
VERSION AX011612.1 GI:9998136
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                                                                                                                                                         Human nucleic acid sequences obtained from pancreas tumor tissue Patent; WO 9955858-A 8 04-NOV-1999; SCHMITT ARKIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN (DE); PILARSKY CHRISTIAN (DE)

LOCATION/Qualifiers
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1020)
                                                                                                                                                                                                                                                 Pilarsky,C.
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106

17 gArgLeuThrGlnGlyArgTrpValArgLySSerArgValAlaMetGluL CCGACTCACACAAGGCAGGTGGGGTGAGGAAATCCAGAGTTGCCATGGAGA 156 34

34 ysIleProValSerAlaPheLeuLeuLeuValAlaLeuSerTyrThrLeu AAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCCTCTCCTACACTCTG 206 50

AlaArgAspThrThrValLysProGlyAlaLysLysAspThrLysAspSe GCCAGAGATACCACAGTCAAACCTGGAGCCAAAAAGGACACAAAGGACTC 256 67

rArgProLysLeuProGlnThrLeuSerArgGlyTrpGlyAspGlnLeuI TCGACCCAAACTGCCCCAGACCCTCTCCAGAGGTTGGGGTGACCAACTCA 306 84

leTrpThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn TCTGGACTCAGACATATGAAGAAGCTCTATATAAATCCAAGACAAGCAAC 100 356

101 LysProLeuMetIleIleHisHisLeuAspGluCysProHisSerGlnAl AAACCCTTGATGATTATTCATCACTTGGATGAGTGCCCACACAGTCAAGC 117 406

117 aLeuLysLysValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluG

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                                                                                                                                                                                                                                                                                                                                                          Human nucleic acid sequences from ovarian tumour tissue patent: WO 9953040-A 265 21-OCT-1999; SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
                                                                                                                                                                                                                                                                                                                                                                                                                   Schmitt, A., Specht, T., Dahl, E., Hinzmann, B.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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Zhang, J.S. and Smit
Direct Submission
                                                                                                                                                                                                            1 (bases 1 to 956)
Zhang, J.S. and Smith,
Human homolog of XAG
                                                                                                                                                                                                                                                                                                                         Homo sapiens putative secreted AF088867
                                                                                                                                        Submitted (30-AUG-1998) Pathology and Lab. 200 SW 1st St., Rochester, MN 55905, USA
                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                              AF088867.1 GI:6652811
                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                    Mammalia;
                                                                                                                                                                                                                                                               Eukaryota;
                                                                                                                                                                                                                                                                                         human.
                                            /note="differentially expressed in tumors; similar
Xenopus cement gland-specific secreted protein"
/codon_start=1
        /product="putative secreted protein
/protein_id="AAF22484.1"
/db_xref="GI:6652812"
                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                    Eutheria;
translation="MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTL/
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Primates;
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AspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (09-DEC-1997) Surgery, Road, MSLS Building, Room P228,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thompson, D.A. and Weigel, R.J
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1 (bases 1 to 1077)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation-"MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTL
SRGWGJQLIWTQTYEEALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAE
QEVLLNLVVETDKHLSPDGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALL
LDNMKKALKLLKTEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="hAG-2/R"
/note="similar to Homo sapiens protein hAG-2/C deposited under GenBank Accession Number AF007791, and to Xenopus laevis cement gland-specific proteins np77 and XAC-2 deposited under GenBank Accession Numbers U82110 and AF025474, respectively"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="hAG-2/R"
59. .586
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/protein_id="AAC82614.1"
/db_xref="GI:3779226"
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/note="isolated from estrogen
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/db_xref="taxon:9606"
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TCTCTATGCTTACGAACCTGCAGATACAGCTCTGTTGCTTGACAACATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACCCATCTCTGACAGTTAGAGCCGATATCACTGGAAGATATTCAAATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAATTGGCAGAGCAGTTTGTCCTCCTCAATCTGGTTTATGAAACAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nLysLeuAlaGluGlnPheValLeuLeuAsnLeuValTyrGluThrThrA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGTGACCAACTCATGTGGACTCAGACATATGAAGAAGCTCTATATAAAT
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                                                                                                                                                                                                                                                                                                                                                                                    Submitted (21-DEC-1998) Laboratory of Medicine and Pathology, Mayo Clinic, 200 SW 1st Street, Rochester, MN 55905, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
2 (bases 1 to 1701)
2 hang, J.S. and Smith, D.I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens XAG-2 homolog long AF115926
                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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Zhang, J.S. and Smith, D.I.
Identification of human h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                        /gene="HPC8"
58. .585
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                                                                                                                                                                                /gene="HPC8"
                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                    ell_type="prostate
.1701
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ORIGIN
                                                                 ACCESSION
VERSION
                                                                                                                                                           seq_documentation_block:
LOCUS BC015503
                                                                                                                                        DEFINITION
                                                                                                                                                                                                                             seq_name:
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                                                                                                                                                                                                                                                                                                   ysLysAlaLeuLysLeuLeuLysThrGluLeu
                                                                                                                                                                                                                                                                                                                                                                   TCTCTATGCTTACGAACCTGCAGATACAGCTCTGTTGCTTGACAACATGA
                                                                                                                                                                                                                                                                                                                                                                                    gLeuTyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetL 196
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Ratio:
                                                                 BC015503
BC015503.1
                                                                                           836 bp mRNA linear
Homo sapiens, anterior gradient 2 (Xenepus laevis)
MGC:9112 IMAGE:3852448, mRNA, complete cae
BC015503
                                                 MGC
    Homo
                         human.
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Gaps:
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                                                                                                                                      homolog,
                                                                                                                                                             PRI 29-OCT-2001
                                                                                                                                        clone
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JOURNAL REFERENCE AUTHORS TITLE

FEATURES

source

gene

/cell

JOURNAL

REFERENCE AUTHORS TITLE

SOURCE ORGANISM

Homo

sapiens

seq\_documentation\_block: seq\_name: gb\_pr:AF115926

502 179 452 163 402 146 352

552 196 302

113 252 202

79

96

152

129

DEFINITION VERSION ACCESSION KEYWORDS

AF115926.1

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REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity: 100.000
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                                               103
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                                                                                         47
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  64
                                                                                                                                                                                                                                                                          14
                                                                                                                                                                                                                           HisProSerArgArgLeuThrGlnGlyArgTrpValArgLysSerArgVa
                                                                                                                                                         lAlaMetGluLysIleProValSerAlaPheLeuLeuLeuValAlaLeuS
ThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGl
                                            CCTACACTCTGGCCAGAGATACCACAGTCAAACCTGGAGCCAAAAAGGAC
                                                                      erTyrThrLeuAlaArgAspThrThrValLysProGlyAlaLysLysAsp
                                                                                                                                      TGCCATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCCCTCT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 20 Row: o Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 665281:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, web site:

http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
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Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Tissue Procurement: ATCC
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Sequence 40 from Patent WO0078960.
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                                                                                                                                                                                                 Compositions and methods
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                                      Jiang,Y., Harlocker,S.L. Compositions and methods
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   Patent: WO 0196388-A 1635 CORIXA CORPORATION (US)
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Mammalia; Eutheria;
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DEFINITION Sequence 61 fi
ACCESSION AR177367
VERSION AR177367.1 G1
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|||||||||
||TTTGTCCTCCCCAATCTGGTTTATGAAACAACTGACAACACCTTTCTC 402
                                                                                                                                                                                                                                                                                                    CCAGAGATACCACAGTCAAACCTGGAGCCAAAAAGGACACAAAGGACTCT
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                                                                                                                                        uProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysAlaLeuLysL
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                                                                                     TGCTGAAGACTGAATTG
        Sequence 61 from patent US 6312922.
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   AR177367.1 GI:17919722
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/db_xref="taxon:9606"
145 c 120 g 13
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1. .593
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AUTHORS
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FEATURES
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SOURCE
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US-09-674-266A-181 x AR177367
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Quality:
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                      etLysLysAlaLeuLysLeuLeuLysThrGluLeu
                                                                                              CysProHisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIl
                                                                                                                                                                                                                                                                                                                            yTrpGlyAspGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrL
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                                                               AATCCAAGACAAGCAAACCCTTGATGATTATTCATCACTTGGATGAG
                                                                                                                                                                                                                                                                                ysSerLysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGlu
            TGAAGAAAGCTCTCAAGTTGCTGAAGACTGAATTG
                                                     TCGTCTCTATGCTTACGAACCTGCAGATACAGCTCTGTTGCTTGACAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 1689) Edwards, J.-B. Dumas. Milne., Duclert, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown
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350 c 335 g
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REFERENCE
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SOURCE
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US-09-674-266A-181 x AX341084
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Percent Similarity: 100.000
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                                                                            SpLySHiSLeuSerProAspGlyGlnTyrValProArgIleMetPheVal 162
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AspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnAr 179
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
143 c 113 g 13
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KEYWORDS
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US-09-674-266A-181 x AX341234
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CORIXA CORPORATION (US)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/db_xref="taxon:9606"
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Sequence 149 from patent US 6
ARIT7410
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AX331601
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                                                                                                      Thompson,D.A. and Weigel,R.J. hAG-2, the human homologue of the Xenopus laevis cement gland gene XAG-2, is coexpressed with estrogen receptor in breast cancer cell
Submitted (10-JUN-1997) Surgery, Stanford, 1
Building, Room P228, Stanford, CA 94305, USA
                          Thompson, D.A.
Direct Submission
                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to Homo sapiens protein hAG-2/R deposited in GenBank Accession Number AF038451, and to Xenopus laevis cement gland proteins np77 deposited in GenBank Accession Number U82110 and XAG-2 deposited in GenBank Accession Number AF025474"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="secreted cement gland /protein_id="AAC77358.1" /db_xref="GI:3779197"
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11. .538
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/cell_type="adenocarcinoma"
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/db_xref="taxon:9606"
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of: US-09-674-266A-181 to:

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Search information block: Query: US-09-674-266A-181 Query length: 206
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-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR.SCORE-pct
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR.SCORE-pct
-THR.MAX-100 -THR.MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFWT-pfs
-NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US09674266_@CGN__10 -NCPU-6 -ICPU-3 -LONGLOG
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sequences: 1736436
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3.9e-96
3.9e-95
2.4e-90
1.8e-90
4.6e-84
3.6e-84
8.0e-75
1.1e-67
7.1e-67
7.1e-67
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4.0e-63
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        2 1.8e-55

7.4e-54

6 7.4e-51

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                                                                   ### AGACTCAGCTGTGCTGGCACACTCAGCGGCTCTGGACCGCATCCTAGCCG
        yslleProValSerAlaPheLeuLeuLeuValAlaLeuSerTyrThrLeu
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seq_documentation_block:
ID AA252865 standard; cl
XX AAZ52865;
XX AAZ52865;
XX Pancreas; tumor; EST;
XX DE19820190-A1.
XX DA19820190-A1.
XX DE19820190-A1.
XX PAR PR-1998; 98DE-:
XX PR 28-APR-1998; 98DE-:
XX PR 28-APR-1998; 98DE-:
XX PR (META-) METAGEN GES (
XX PR P-PSDB; AAY73835, AAY
XX PPT New human nucleic ac
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US-09-674-266A-181 x AAZ52865
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH83168 +
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:ABK09584 -
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:ABK15919 +
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA77841 +
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                                                            Align seg 1/1 to:
                                                                                                                                                                                                             Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes novel polypeptides and their encoding nucleic acids derived from human pancreatic tumor tissue which have cytostatic activity. The sequences are also useful in producing pharmaceutical compositions for treatment of pancreatic tumors. AAZ52858-Z53014 represent expressed sequence tag (EST) fragments derived from a human pancreatic tumor cDNA library and which encode the proteins represented
                                                                                                                                                                                                                                                                                                                                                                                                                                                           represent expressed se pancreatic tumor cDNA in AAY73814-Y74252.
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P-PSDB; AAY73835, AA
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1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerAr
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Ratio: 5.160
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- 535.00 1040.7;
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1.5e-47
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9.6e-50
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156 34 106

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seq_documentation_block:
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08-MAR-1999;
02-JUN-1999;
23-JUN-1999;
                                                                                                                                                                                     proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosuppressive; immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; angiogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastoccelic disorder; epithelial disorder; stromal disorder; blastoccelic disorder;
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                                                          06-JAN-2000; 2000WO-US00376
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                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                tumour;
                                                                                                                                                                                                                                                                                                                                             (first entry)
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99WO-US12252.
99WO-US12252.
99US-0141037.
                                                                                                                                                                                                                                                                 diagnosis; neoplastic disease; neoplastic cell growth; tumourigenesis; identification; cancer; cytostatic;
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alignment\_block: US:09-674-266A-181

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AAC58380

Percent Similarity:

Align seg 1/1 to: AAC58380 from:

to:

920

155

34

ysIleProValSerAlaPheLeuLeuLeuValAlaLeuSerTyrThrLeu

50

15,

204

ANATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCCCTCTCCTACACTCTG

105

1 56 17

gArgLeuThrGlnGlyArgTrpValArgLysSerArgValAlaMetGluL

34

17

CCGACTCACACAAGGCAGGTGGGGTGAGGAAATCCAGAGTTGCCATGGAGA

ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerAr

AGACTCAGCTGTGCTGGCACACTCAGAAGCTT.GGACCGCATCCTAGCCG

205

rArgProLysLeuProGlnThrLeuSerArgGlyTrpGlyAspGlnLeuI

84

67

254

alignment\_scores:

Quality:

Ratio:

1025.00 5.025 99.029

Percent Identity: 98

Length:

206 0 .544

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CC The present invention describes an isolated antibody that binds to CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO355, CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, CC PRO1025, PRO1097, PRO1097, PRO1107, PRO1152, PRO11097, PRO1111, PRO1152, PRO1182, PRO1182, PRO1187, PRO1197, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUL-1999;
26-JUL-1999;
30-NOV-1999;
20-DEC-1999;
05-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thirty PRO polynucleotides encoding treatment, diagnosis and prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 50; Fig 27; 286pp; English.
Sequence 920 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ashkenazi AJ,
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                                            present invention.
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99US-0145698.
99WO-US28313.
99WO-US30911.
2000WO-US00219.
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296
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231 T;
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  other;
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255

304

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seq_documentation_block:
ID AAZ77486 standard; cD
XX
AC AAZ77486;
XX
DT 10-APR-2000 (first e
XX
Expressed sequence ta
KW Expressed sequence ta
KW Expressed sequence ta
KW Expressed sequence ta
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DE19817557-A1.
XX
DE19817557-A1.
XX
OS Homo sapiens.
XX
PN DE19817557-A1.
XX
OS HOMO SAPR-1999;
XX
OS HOMO SAPR-1998;
PD 21-OCT-1999.
XX
OS HOMO SAPR-1998;
PF 09-APR-1998;
PF 09-APR-1998;
PF 09-APR-1998;
PF 09-APR-1998;
PF NESSENTHAL A, Specht
XX
PP 1 ROSENTHAL A, Specht
XX
PP 1 PSDB; AAY76590.
XX
NEW Nucleic acid sequention of the
XX
New nucleic acid sequention of the
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Claim 3; Page 167; 31
XX
This invention descri
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                                                       New nucleic acid sequences expressed in ovarian, tissues, and derived polypeptides, for treatment identification of therapeutic agents
                                                                                                                                                                                                                                                                                                                                               Expressed sequence tag; EST; human; ovarian tumor; anticancer; gene therapy; treatment; ss.
                                                                                                                                                                                                                                                                                                                                                                                           Human ovarian tumor cDNA library derived EST fragment 37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ77486 standard; cDNA; 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184
                              Claim 3; Page 167; 310pp; German.
                                                                                                               WPI; 1999-591920/51.
P-PSDB; AAY76590.
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ovarian cancer and
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CC have anticancer activity and are highly expressed in ovarian tumor CC tissue (and some also in testis and breast cancer tissue). The products of the invention can be used for gene therapy. (A) are used (i) for recombinant expression of polypeptides (B) and (ii) to isolate complete (C genes. (B) are used (i) to identify agents suitable for treatment of (c ovarian cancer; (ii) directly for treating this form of cancer (C (including expression from gene therapy vectors) and (iii) for generation (c of specific antibodies. (A) are identified by assembling ESTs (expressed (c sequence tags) from a particular tissue type before comparison of (c expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated (c with the fact that ESTs from different libraries may represent different (C parts of the same unknown gene, distorting the estimated frequency of cocurrence in a particular tissue. AA77450-Z77572 represent the human (c) of the invention and encode the protein fragments represented in the method (c) the invention and encode the protein fragments represented in
   212
   216
0 other;
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Sequence 1018 BP; 343 Α, ე G; 247 T;

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alignment_block:
                                                                                                                                                                   alignment_scores:
                                                                                             US-09-674-266A-181 x AAZ77486
                                                                     Align seg 1/1 to: AAZ77486
                                                                                                                                 Percent Similarity:
17
                       57
                                            1 ArgLeuSerCysAlaGlyThrLeuSerGlySer.GlyProHisProSerA
                     AGACTCAGCTGTGCTGGCACACTCAGA...AGCTTGACCGCATCCTAGCC
                                                                                                                                           Quality:
Ratio:
                                                                                                                               1018.50
5.017
98.068
                                                                     from: 1
                                                                                                                                 Percent
                                                                                                                                Identity:
                                                                     to:
                                                                       1018
                                                                                                                                            Gaps:
                                                                                                                                 98.068
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2
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33
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454
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                                           nLysProLeuMetIleIleHisHisLeuAspGluCysProHisSerGlnA 117
                                                                                                                                                                                                                                                                                                      IleTrpThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAs 100
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hrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeuTyrAlaTyr
                                                                                                     GlnPheValLeuLeuAsnLeuValTyrGluThrThrAspLysHisLeuSe
                                                                                                                                                                                                                                                                                                                                                               erArgProLysLeuProGlnThrLeuSerArgGlyTrpGlyAspGlnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                            uAlaArgAspThrThrValLysProGlyAlaLysLysAspThrLysAspS
                                                                                                                                                                 CTTTAAAGAAAGTGTTTGCTGAAAATAAAGAAATCCAGAAATTGGCAGAG
                                                                                                                                                                             laLeuLysLysValPheAlaGluAsnLysGluIleGlnLysLeuAlaGlu
                                                                                                                                                                                                                            CAAACCCTTGATGATTATTCATCACTTGGATGAGTGCCCACACAGTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                           GGCCAGAGATACCACAGTCAAACCTGGAGCCAAAAAGGACACAAAGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCCCTCTCCTACACTCT
                                                                                                                                                                                                                                                                                       ATCTGGACTCAGACATATGAAGAAGCTCTATATAAATCCAAGACAAGCAA
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This invention describes novel nucleic acid (cDNA) sequences (A) which

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seq_documentation_block:
ID AAV29047 standard; cD
XX AAV29047;
XX 21-AUG-1998 (first e
XX Human protein compris
XX Human protein compris
XX Human protein; secret
KW Human protein;
XX Homo sapiens.
XX Chemokinetic; thrombo
XX Homo sapiens.
XX Homo
                      alignment_scores:
Quality:
Ratio:
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                                                                                                                                                                                                            This is the nucleotide sequence of a novel human protein comprising a secretory signal isolated from stone ancer cells. Its proteins can be used as nutritional sources or supplements. The proteins may also have cytokine functions, immune modulating functions, haematopoiesis regulating activity, activinyinhibin regulating activity, activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein; secretory signal; nutritional source; cytok immunity; haematopoiesis; activin; inhibin; tumour; chemota chemokinetic; thrombolytic; anti-inflammatory; inhibition; stomach cancer cell; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Pages 114-116; 131pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human proteins with simmune deficiencies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human protein comprising secretory signal nucleotide sequence
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(SAGA) SAGAMI CHEM RES CENTRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity:
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DB; AAW37872.
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5.169
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73.600
74.600
/*tag- a "human protein comprising secretory signal"
                                                                                                                                                                 275
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seq_documentation_block:
ID AAH35026 standard; cl
XX
AC AAH35026;
XX
DT 03-SEP-2001 (first 6
XX
AC Human colon cancer an
XX
KW Human; colon cancer;
KW colorectal carcinoma.
XX
OS Homo sapiens.
XX
PD W0200122920-A2.
XX
PD 05-APR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                513 CCGTCTCTATGCTTACGAACCTGCAGATACAGCTCTGTTGCTTGACAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 ValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAs 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            413 CTGACAAACACCTTTCTCCTGATGGCCAGTATGTCCCCCAGGATTATGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 hrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMetPhe
                                                                                                                                  colorectal carcinoma;
                                                                                                                                                     Human; colon cancer;
                                                                                                                                                                                     Human colon cancer antigen encoding cDNA SEQ ID NO:2108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 AATCCAAGACAAGCAACAAACCCTTGATGATTATTCATCACTTGGATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 TTGGGGTGACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 AAGGACACAAAGGACTCTCGACCCAAACTGCCCCAGACCCTCTCCAGAGG
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                                                                                                                                                   cancer antigen; diagnosis; detection;
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alignment_block:
US-09-674-266A-181 x AAH35026
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                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AAH35026 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention diagnosis and treatment of diseases associated with inappropriate P
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03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
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                erLysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGluCys
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                                                                                                                                        AspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTr 79
                                                                                                                                                                                                                                                                                                   gValAlaMetGluLysIleProValSerAlaPheLeuLeuLeuValAlaL 46
CCAAGACAAGCAACAAACCCTTGATGATTATTCATCACTTGGATGAGTGC
                                                                   GGGTGACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAAAT
                                                                                       pGlyAspGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrLysS
                                                                                                                                                                                                                                                                                  AGTTGCCATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCC
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seq_documentation_block:
ID AAV19155 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      526
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                                                New isolated human XAG growth factor(s) - used to develop products for treating e.g. liver, lung or breast diseases or hyperproliferative disorders, e.g. cancer.
                                                                                                     WPI; 1998-169093/15
                                                                                                                                                                                                                                                                                                                                                                                                         Human XAG
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                                                                                                                                                                    23-AUG-1996;
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131..595
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This cDNA clone codes for huXAG-1 (see AAW37844), a member of a novel family of human growth factors also including huXAG-2 (see AAW37845)

Claim 5; Fig 1; 141pp; English.

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Colon cancer specific gene (CCSG), provides a molecular marker for CC colon cancer. huXAG-1 cDNA was isolated from a cDNA library CC derived from human colon cancer tissue. Vectors, host cells, and streening methods for identifying agonists and CC antibodies, and screening methods for identifying agonists and CC antagonists of huXAG-1 are provided. HuXAG polypeptides are growth CC factors and can be used to stimulate proliferation of cells. They CC can be used to stimulate the proliferation and differentiation of CC such as fulminant liver failure caused by cirrhosis, liver damage CC caused by viral hepatitis and toxic substances. They can also be used to stimulate or promote liver regeneration, e.g. after consist and pathologies CC suggery. They can also be used to prevent and heal damage to the CC suggery. They can also be used to prevent and heal damage to the CC simulate proliferation and differentiation and promote the repair CC treat acute or chronic lung damage, e.g. emphysema, which results CC in the progressive loss of alveoli, and inhalation injuries, e.g. CC treat acute or chronic lung damage, e.g. emphysema, which results CC in the progressive loss of alveoli, and inhalation of breast tissue and could therefore be used to promote healing of breast tissue constituted to promote the proliferation and differentiation of breast tissue constituted to promote the aling of breast tissue constituted to promote the aling of breast tissue constituted to promote the proliferative disorders, including cancer, in colon cancer. The products can also be used for detection and collaboration cancer, in the proliferative disorders, including cancer, in the cancer, in the proliferative disorders, including cancer, in the proliferative disorders including cancer, in the proliferative disorders including cancer, in the proliferative disorders including cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 875
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                                                                                                                                                                                                                                ProH1sProSerArgArgLeuThrGlnGlyArgTrpValArgLysSerAr
CCACACAGTCAAGCTTTAAAGAAAGTGTTTGCTGAAAATAAAGAAATCCA
                        ProHisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleG1 129
                                                                                                                 CCAAGACAAGCAACCAAACCCTTGATGATTATTCATCACTTGGATGAGTGC
                                                                                                                                          erLysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGluCys 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGATTCCTAGCCGCCGACTCACACAAGGCAGGTGGGTGAGGAAATCCAG
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99.485
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Gaps: 0
Percent Identity: 99.485
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(HUMA-) HUMAN GENOME SCI INC

Ebner R,

Endress GA;

96US-0024347

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seq_documentation_block:
ID AAF63314 standard; cl
XX AAF63314;
XX AAF63314;
XX AAF63314;
XX DT 04-MAY-2001 (first (
XX Human huXAG-1/CCSG co
XX Human; growth factor
KW cell proliferation;
KW hepatitis; cancer; co
XX Homo sapiens.
XX US6171816-B1.
XX US6171816-B1.
XX 22-AUG-1997; 97US-
XX 23-AUG-1996; 96US-
PR 23-AUG-1997; 97US-
XX 23-AUG-1997; 97US-
XX PF 22-AUG-1997; 97US-
XX NOWEL HUMAN GENOME
XX WPI; 2001-136872/14
DR P-PSDB; AAB72203.
XX Novel human growth |
PT treating colon cance
PT treating colon cance
PT the lungs and for 10
XX Novel human growth |
PT treating colon cance
PT treating colon cance
PT treating colon cance
PT treating colon cance
CC known as a colon ca
CC claim 45; Fig 1; 59
XX This invention rela
CC known as a colon ca
CC proliferation of ce
proliferation of ce
promoting damage to
CC cancer, in particul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; growth factor; huXAG-1; colon cancer specific gene; CCSG; cell proliferation; liver disease; fulminant liver failure; cirrhosis; hepatitis; cancer; colon cancer; colorectal carcinoma; ss.
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CC rhis invention relates to a human growth factor polypeptide huXAG-1 also CC known as a colon cancer specific gene (CCSG). HuXAG-1 stimulates cell CC proliferation as a growth factor. The HuXAG-1 protein is useful for CC identifying compounds capable of enhancing or inhibiting cellular CC response induced by huXAG-1. The protein is also useful for stimulating CC proliferation of cells e.g. colon, breast, liver and lung cells, and CC hepatocytes. It is useful for alleviating or treating liver diseases and CC pathologies such as fulminant liver failure caused by cirrhosis, liver CC damage caused by viral hepatitis and toxic substances, for preventing and CC treating damage to the lungs caused by various pathological states and CC cancer. HuXAG-1 and the identified antagonist are useful for treating cancer in particular colon cancer. Detecting altered levels of huXAG-1 and its polynucleotides are useful for diagnosing or detecting cancer in mammals. The gene encoding huXAG-1 is useful for monitoring human Novel human growth factor polypeptide useful for diagnosing and treating colon cancer and liver diseases, to prevent and heal damage to the lungs and for identifying modulators of therapeutic use  $\dot{\cdot}$ Fig 1; 59pp; English.

SSSSS

Sequence

875

BP;

283

189

180

223 Τ;

0 other;

colorectal chromosome

carcinoma. huXAG-1 nucleic acid molecules are also useful for identification. The present sequence represents cDNA encoding

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seq_documentation_block:
ID    AAV59320 standard; cl
XX
AC    AAV59320;
XX
DT 21-DEC-1998 (first of the control of the co
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alignment_block:
US-09-674-266A-181
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                                                                                                      109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated mucous-associated polypeptide, zsig10 - used to develop products for treating e.g. tumour metastasis, microbial infections, cystic fibrosis, asthma, bronchitis or inflammatory bowel disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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ThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGl
                                                                                                      lAlaMetGluLysIleProValSerAlaPheLeuLeuLeuValAlaLeuS
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seq_documentation_block:
ID AAP44884 standard; cI
XX AAF44884;
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XX DT 28-MAR-2001 (first &
XX DT 28-MAR-2001 (first &
XX DT 28-MAR-2001 (first &
XX Human; breast cancer;
XX Human; breast concer;
XX PD 28-DEC-2000.
XX WO200078960-A2.
XX PP 23-JUN-199; 99US-1-
XX PP 23-JUN-1999; 99US-1-
XX PP 23-JUN-1999; 99US-1-
XX CORI-) CORIXA CORP.
XX PP Yuqiu J, Mitcham JL
XX CORI-) CORIXA CORP.
XX The prevention, treatmen
XX Claim 25; Page 132;
XX The present inventio
CC Dreast cancer relate
CC against, diagnosis o
CC cancer.
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                                    The present invention provides the coding sequences for a number of breast cancer related proteins. These can be used in vaccinations against, diagnosis of and treatment of cancer, particularly breast
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                                                                                                   Claim 25; Page 132; 165pp; English.
                                                                                                                                    New polynucleotides encoding breast tumor specific proteins, useful prevention, treatment and diagnosis of breast cancer -
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fingerprint identification

technique;

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alignment_scores:
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13-APR-1998;
10-AUG-1998;
04-SEP-1998;
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98US-0081563.
98US-0096116.
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ID AAZ40846 standard; DN
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XX Secreted protein EST
XX Secreted protein; fin
KW Secreted protein; fin
KW chromosome mapping; h
KW hyperlipidaemia; card
KW renal injury; amino a
XX renal injury; amino a
XX W hypertension; ss.
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PR 04-SEP-1998; 98US-0
PR 13-APR-1998; 98US-0
PR 11-AUG-1998; 98US-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome mapping; human; hereditary disease; diagnosis; cancer; hyperlipidaemia; cardiovascular; neurodegenerative disorder; therapy; autoimmune disease; rheumatic disease; embryogenic disorder; myopathy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used to clone upstream genomic DNA sequences including promoters. This is in turn useful for identifying proteins that interact with promoter sequences. Some of the proteins may be useful in diagnosing and treating several disorders including, but not limited to: cancer, hyperlipidaemia, cardiovascular and neurodegenerative disorders, autoimmune diseases, and rheumatic diseases, embryogenic disorders, hypertension, renal injury, amino acidurias, hypoglycaemia, male rat infertility and myopathies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence encodes a human secreted protein of the invention. The extended CDNAs (Or genomic DNAs obtainable from them) may be used to prepare PCR primers and probes. These are useful for forensic matching or positive identification by DNA sequencing. They may also be used in alternative fingerprint identification techniques. Antibodies against the proteins encoded by the extended cDNAs are useful in identification of tissue types or cell species, as well as identifying tissue specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                soluble proteins. The sequences can be used for chromosome mapping and identification of genes associated with hereditary diseases or drug response. Signal sequences from the cDNAs can be used in construction of secretion vectors. Other sequences derived from the extended cDNAs can be
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                                                                                        נם
                                                                                          breast cancer
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The invention describes the novel use of a protein found in breast cancer cell membranes (BCMP 7) for diagnosing, preventing and treating breast cancers. The peptide has cytostatic action and potential uses in gene therapy and in vaccines. The polypeptide, antisense nucleic acids, or fusion proteins comprising and Green Fluorescent protein or the DsRe Fluorescent protein, antibodies specific for and/or nucleic acid are

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seq_documentation_block:
ID     AAV29048 standard; ct
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AC      AAV29048;
XX
DT     21-AUG-1998 (first e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used for the prevention and/or treatment of breast cancer. Antibodies against may also be used for screening for and/or diagnosis of breast cancer in a patient. The method for monitoring/assessing breast cancer treatment in a patient and for the identification of metastatic breast cancer cells in samples from a patient. This sequence encodes breast cancer cell associated protein 7 (BCMP 7), located on chromosome 7p21.3, described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                    rAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMetPheV 162
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                                                                                                                                                   GAAGAAAGCTCTCAAGTTGCTGAAGACTGAATTG
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alignment_scores:
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Ratio: 5.137
Percent Similarity: 100.000
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                                                                                                                                                                                             US-09-674-266A-181 x AAV29048
                                                                                                                                                                                                                                                                                                                            This is the nucleotide sequence of the open reading frame of a novel human protein comprising a secretory signal (AAV3047), isolated from stomach cancer cells. Its proteins can be used as nutritional sources or supplements. The proteins may also have cytokine functions, immune modulating functions, haematopoiesis regulating activity, activiny/inhibin regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein; secretory signal; nutritional source; cytok immunity; haematopolesis; activin; inhibin; tumour; chemota chemokinetic; thrombolytic; anti-inflammatory; inhibition; stomach cancer cell; ds.
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                         101
                                                                                                                                                                                                                                                                                                       Sequence 525 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human proteins with secretory signal sequences - used to treat immune deficiencies, infections, tumours, and haematopoietic
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GlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrLysSerLysTh
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DB; AAW37872.
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cancer. The polypeptides and monoclonal antibodies specific for t polypeptides can also be used to inhibit the development of lung Agents which bind the polypeptides can be used for detecting lung and for monitoring the progression of lung cancer.

lung cancer

cancer.

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seq_name:
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 The invention provides isolated human lung tumor nucleic acids and polypeptides. The polypeptides can be used for the treatment of lung cancer. The polypeptides and polynucleotides can be used to stimulate cells or antigen presenting cells for use in the treatment of lung
                                                                                                                                                                                                                                                                                                                                                                                                           501
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                                                                                                                                                                                                                                                                                                       Human lung tumor associated polynucleotide.
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                                                Claim 1; Page 90; 148pp; English
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                                                                           isolated lung tumor polynucleotides, treatment, prevention and monitoring
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98US-0040984.
98US-0123912.
98US-0123933.
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                                                                                                                                                                                                                                                                                                                                                              CDNA;
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AAC65817 standard;
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21-FEB-2001

(first entry)

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Ratio:
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17-DEC-1999;
30-DEC-1999;
10-JAN-2000;
22-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polypuncleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit development of cancer.
152
                                              102
                                                                                                                                                                                                                                                                                                                                     Sequence 793 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1a; Page 123; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polypeptide comprising an immunogenic portion of a lung protein is used for detecting and monitoring progression of lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-APR-2000; 2000WO-US08896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lung cancer; therapy; treatment;
vaccine; detection; ss.
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                                             ThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGl
ACAAAGGACTCTCGACCCAAACTGCCCCAGACCCTCTCCAGAGGTTGGGG
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99US-0466396.
99US-0476496.
2000US-0480884.
2000US-0510376.
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                                                  uTyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysL
||||||||||::: |||||||||
| CTATGCTTACAAACT.GCAGATACGCTCTGTTGCTTGACACAT...GAAA
                                                                                                                          ProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLe
                                                                                                                                                                  ACACCTTTCTCCTGATGGCCAGTATGT.CCCAGGATTATGTTTGTCAC
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-Q=/cgn2_1/USPTO_spool/USO9674266/runat_08102002_093325_26183/app_query.fasta_1.271
-DB=Issued_Patents_Na, -QFWT=fastap -SUFFIX=p2n.rni
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -QGAPOP=4.500 -OGAPEXT=0.050 -VGAPOP=10.000
-YGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
-THR_SCORE-pct -THE_MAX=100 -THE_MIN=0 -AALIGN=15 -MODE=LOCAL
-OUTFMT=pfs -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=200000000
-USER=US09674266_@CGN1_1_46 -NCPU=6 -ICPU=3 -LONGLOG
-USER=US09674266_@CGN1_1_46 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
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Cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-04/0-984-78+ 856.
Cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-04/0-984-78+ 856.
Cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-123-912-78+ 856.
Cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-916-576B-35+ 642.
Cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-916-576B-36+ 487.
Cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-916-576B-96+ 458.
Cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-916-576B-10+ 376.
Cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-916-576B-37+ 253.
Cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-910-000-607-209+ 252.
Cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-916-576B-3+ 222.
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Cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-916-576B-19+ 158.
Cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-916-576B-11+ 104.
Cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-916-576B-11+ 104.
Cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-916-576B-11+ 104.
Cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-916-576B-13+ 104.
Cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-916-576B-13+
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                                                                                  MB. seq: US-08-916-576B-18 + MB. seq: US-08-916-576B-16 + MB. seq: US-08-916-576B-14 - MB. seq: US-08-311-363-14 - MB. seq: US-08-311-363-12 - MB. seq: US-08-311-363-12 - MB. seq: US-08-311-363-12 - MB. seq: US-08-23-305-8 - MB. seq: US-08-249-386-8 - MB. seq: US-08-249-386-8
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    Quality:
                                                                                                                             alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: US-08-916-576B-1
    Align seg 1/1 to:
                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                          Ratio:
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        US-08-916-576B-1
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seq_documentation_block:
; Sequence 1, Application
; Patent No. 6171816
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US-09-674-266A-181 x US-08-916-576B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2500
TELEPHONE: (202) 371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,347
FILING DATE: 23-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOYEL HUMAN GROWTH FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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CITY: WASHINGTON
STATE: DC
COUNTRY: US
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
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131..595
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Percent Identity:
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GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Complementary DNAs
FILE REFERENCE: GENSET: 021A
CURRENT APPLICATION NUMBER: 05/09/247,155A
CURRENT FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/04,121
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/096,273
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-08-10
EARLIER PILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
SEQ ID NO 61
LENGTH: 1689
                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-247-155-61
                                                                                                                                                                                                                                                                                             Sequence 61, Application US/09247155A Patent No. 6312922
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alignment_scores:
    Quality:
    Ratio:
Percent Similarity:
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; LOCATION: 1674..1689
US-09-247-155-61
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FEATURE:
NAME/KEY:
LOCATION:
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LOCATION: 51.110
OTHER INFORMATION: Soon Heijne matrix
OTHER INFORMATION: score 11.2
OTHER INFORMATION: seq AFLLLVALSYTLA/RD
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CCCTCTCCTACACTCTGGCCAGAGATACCACAGTCAAACCTGGAGCCAAA
                                                                                                                                             rArgValAlaMetGluLysIleProValSerAlaPheLeuLeuValA
                                                GTTGACCCATCTCTGACAGTTAGAGCCGATATCACTGGAAGATATTCAAA
                                                            ValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAs
                                                                                                CTGACAAACACCTTTCTCCTGATGGCCAGTATGTCCCCAGGATTATGTTT
                                                                                                           hrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMetPhe
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alignment_scores:
Quality:
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US-09-674-266A-181 x US-09-247-155-149
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APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Complementary DNAS
FILE REFERENCE: GENSET.021A
CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/096,273
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
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                                                                                                                                                                                                                            Align seg 1/1 to: US-09-247-155-149
                                                                                                                                                                                                                                                                                                                        Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patent.pm
SEQ ID NO 149
LENGTH: 940
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APPLICANT: Dumas Mi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 149, Application US/09247155A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 11.1999998092651
OTHER INFORMATION: seq AFLLLVALSYTLA/RD
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LOCATION: 177..569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: sig_peptide
LOCATION: 177..236
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gArgLeuThrGlnGlyArgTrpValArgLysSerArgValAlaMetGluL
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seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-040-984-78
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                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Wang, TongTong
TITLE OF INVENTION: COMPOUND:
TITLE OF INVENTION: OF LUNG
NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 78, Application US/09040984 Patent No. 6210883
ATTORNEY/AGENT INFORMATION:
NAME: Maki. David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version
CURRENT APPLICATION DATA:
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                                                                                                     APPLICATION NUMBER: FILING DATE: 18-MAF CLASSIFICATION:
                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 98104
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                                                                                                                                                                                                                                                                                                                                                     SEED and BERRY LLP
                                                                                                                                                                                                                               Diskette
                                                                                                                         18-MAR-1998
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OF LUNG CANCER
                                                                                                                                         US/09/040,984
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alignment_block:
US-09-674-266A-181 x US-09-040-984-78
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seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-123-912-78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                               TGCCATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCCCTCT
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                                              ysAlaLeuLysLeuLeuLys 203
                                                                                         CTATGCTTACAAACT.GCAGATACGCTCTGTTGCTTGACACAT...GAAA
                                                                                                        uTyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysL 197
                                                                                                                                                                                                                                                                                                                                                                                        AGACAAGCAACAAACCCTTGATGATTATTCATCACTTGGATGAGTGCCCA 301
                                AAGCTCTCAAGTTGCTNAAA
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seq\_documentation\_block:
 Sequence 78, Applicati

Application US/09123912A

Percent Similarity:

Ratio:

Gaps: 1 Percent Identity: 93.684

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; OTHER INFORMATION: Where n
; NAME/KEY: modified_base
; LOCATION: (765)
; OTHER INFORMATION: Where n
; NAME/KEY: modified_base
; LOCATION: (787)
; OTHER INFORMATION: Where n
US-09-123-912-78
                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Pat
SEQ ID NO 78
LENGTH: 793
TYPE: DNA
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GENERAL INFORMATION:
                                                                                                                                                                               NAME/KEY: modified_base
LOCATION: (732)
OTHER INFORMATION: Where n i
NAME/KEY: modified_base
LOCATION: (740)
OTHER INFORMATION: Where n i
NAME/KEY: modified_base
LOCATION: (748)
OTHER INFORMATION: Where n i
NAME/KEY: modified_base
LOCATION: (758)
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NAME/KEY: modified_base
LOCATION: (660)
OTHER INFORMATION: Where n
NAME/KEY: modified_base
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OTHER INFORMATION: Where n
NAME/KEY: modified_base
LOCATION: (492)
OTHER INFORMATION: Where n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Reed, Steven G.
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOUNDS AND METHODS
FILE REFERENCE: 210121.455C1
CURRENT APPLICATION NUMBER: US/09/123,912A
CURRENT FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                   LOCATION: (710)
OTHER INFORMATION: Where n
NAME/KEY: modified_base
LOCATION: (711)
OTHER INFORMATION: Where n
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PRIOR FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 114
                                                                                                                                                  OTHER INFORMATION: Where NAME/KEY: modified_base LOCATION: (762)
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OTHER INFORMATION: Where NAME/KEY: modified_base
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: LENGTH: 401
: TYPE: DNA
: ORGANISM: Human
US-09-221-298-32
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; Sequence 32, Application
; Patent No. 6284241
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US-09-674-266A-181 x US-09-123-912-78
                                                                        PATENT NO. JULIAGE HOLDS AND METHODS FOR THERAPY AND APPLICANT: XL, Jiangchun
APPLICANT: XL, Jiangchun
APPLICANT: XL, Jiangchun
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND TITLE OF INVENTION: OF COLON CANCER
FILE REFERENCE: 210121.471
CURRENT APPLICATION NUMBER: US/09/221,298
CURRENT FILING DATE: 1998-12-23
CURRENT FILING DATE: 1998-12-23
CURRENT FILING DATE: 1998-12-33
CHARLEST OF SEO ID NOS: 112
                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-221-298-32
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                                                            SOFTWARE: FastSEQ for Windows Version SEQ ID NO 32
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alignment_block:
US-09-674-266A-181 x US-09-221-298-32
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 35, Application Patent No. 6171816 GENERAL INFORMATION:
CLASSIFICATION: 536 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                   APPLICANT: YU, GUO-LIANG
APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                352
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                                                              CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                        STATE: DC
COUNTRY: US
ZIP: 20005-3934
                                                                                                                                                                                                                      STREET: 1100 NEW CITY: WASHINGTON
                                                 FILING DATE
                                                                                                                                                                                                                                       ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L. STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProArgIleMetPheValAspProSerLeuThrValArgAla.AspIleT
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FILING DATE:

23-AUG-1996

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seq_documentation_block:
   Sequence 5, Application US/08916576B
   Patent No. 6171816
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    Quality:
    Ratio:
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; MOLECULE TYPE:

US-08-916-576B-35
                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-916-576B-5
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REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 386 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-08-916-576B-35 from: 1
                GENERAL INFORMATION:
APPLICANT: YU, GUO-LIANG
APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
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NAME: STEFFE, ERIC K.
CORRESPONDENCE ADDRESS:
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; LOCATION:
; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-916-576B-5
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                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-08-916-576B-5 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 732 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                  US-09-674-266A-181 x US-08-916-576B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 60/024,347
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                 107 sHisLeuAspGluCysProHisSerGlnAlaLeuLysLysValPheAlaG
                                                                                                                                      146 CACTCTCAAGAGGATGGGGAGATGACATCACTTGGGTACAAACTTATGAA
                                                                   196 GAAGGTCTCTTTATGCTCAAAAAAGTAAGAAGCCATTAATGGTTATTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                          123 A.....
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                                                                                    91 GluhlaLeuTyrLysSerLysThrSerAsnLysProLeuMetIleIleHi 107
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/916,576B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C. STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                             sProGlyAlaLysLysAspThrLysAspSerArgProLysLeuProGlnT 74
CTCTTACTCGTCACAGTTTCTTCCAACCTTGCC.....ATTGCAATAAA
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Ratio:
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(202) 371-2540
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49..546
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118..546
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49..117
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3.801
87.425
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Percent Identity: 64.671
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seq_documentation_block:
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US-08-916-576B-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3
                                                                                                                                                                                               CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,347
FILING DATE: 23-AUG-1996
ATTORNEY/ACENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                  TELEFAX: (202) 371-25
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release $1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/916,576B
                                                                                                                                               REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: YU, GUO-LIANG
APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 373 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          396
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            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & STREET: 1100 NEW YORK AVENUE, SUITE 600
                                TOPOLOGY:
                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                           FILING DATE:
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o. 6171816
                                                              nucleic acid
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                                              single
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alignment_block:
US-09-674-266A-181 x US-08-916-576B-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-916-576B-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/08916576B Patent No. 6171816
               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: YU, GU
                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GC
STREET: 1100 NEW YORK AVENUE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
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                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                         CITY: WASHINGTON STATE: DC
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                                                                                                                                                                                                                                                                                                        ZIP:
                                                                                                                                                                                                                                                                                                                          COUNTRY:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             erGlnAlaLeu...LysLysValPhe 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThr. 98
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                                                                                                                                                                                                                                                                                                      20005-3934
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                                                                                             US 60/024,347
                                                                                                                                                                    US/08/916,576B
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1488.0500001
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Gaps:
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seq_documentation_block:
; Sequence 10, Application US/08916576B
; Patent No. 6171816
; GENERAL INFORMATION:
APPLICANT: YU, GUO-LIANG
; APPLICANT: EBNER, REINHARD
APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-674-266A-181 x US-08-916-576B-9
                                                                                                                                                                  seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-916-576B-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-08-916-576B-9 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                              371
                                                                                                                                                                                                                                                                                               136 l.LeuLeuAsnLeu.ValTyrGluThrThrAspLysHisLeuSerProAs 152
                                                                                                                                                                                                                                                                                                                                                                                                                            286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 371-2600
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                                                                                                                                                                                                      NTGGNCNATTTTTCCCCCGGNTTTTTTTTTTTTGGCCCCC
                                                                                                                                                                                                                                        pGlyGlnTyrValProArgIleMetPheValAspPro 164
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3.728
74.096
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Identity: 70.482
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 506 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,576B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                          164
                                                                                                                                                                        146 pLysHisLeuSerProAspGlyGlnTyrValProArgIleMetPheValA 163
                                                                                                                                                                                                                                      114
                                                                                                                                                                                                                                                                                                                                      113 oHisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleGlnL 130
264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                14 AAGACAAGCAACAAACCCTTGATGATTATTCATCANTTGGATGAGTGCCC
                                                                                                                                                                                                                                                                                                                  64 ACACAGTCAAGCTTTAAAGAAAGTGTTTGCTGAAAATAAAGAAATCCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                  97 LysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGluCysPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1100 NEW CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                       ysLeuAlaGluGlnPheValLeuLeuAsnLeuValTyrGluThrThr.As
                                  nArgLeuTyrAlaTyr 183
                                                                                                                                                          CAAACACCTTTCTCCTGATGGCCAGTATGTNCCCAGGGTTATGTTTGTTG
                                                                                                                                                                                                                                      AATTGGCAGAGCAGTTTGTCCTCCTCAATCTGGTTTATGAAACAACTGGA
CGTNNCTTATGCTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
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4.482
93.333
279
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3
87.778
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                                                                                                                                                          213
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seq\_name: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:US-08-916-576B-37

seq\_documentation\_block:

Sequence 37, Application US/08916576B Patent No. 6171816

YU, GUO-LIANG

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alignment_block:
US-09-674-266A-181 x US-08-916-576B-37
                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                       Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-916-576B-37 from: 1 to: 158
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APPLICANT: YU, GUO
APPLICANT: DILLON,
APPLICANT: EBNER,
APPLICANT: ENDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202) 371-25
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/024,347
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rclease #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 158 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
                                                                    106
 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                   65
                                                                                                       48
                                                                                                                                           56
                                                                                                                                                           31 aMetGluLysIleProValSerAlaPheLeuLeuLeuValAlaLeuSerT 48
                                                                                                                                                                                                                                15 ProSerArgArgLeuThrGlnGlyArgTrpValArgLysSerArgValAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/916,576B FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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                                                                    AAG 158
                                   Lys 65
                                                                                                                                           CATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCCCTCTCCT 105
                                                                                                                                                                                                             CCTAGCCGCCGACTCACACAAGGCAGGTGGGTGAGGAAATCCAGAGTTGC 55
                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
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EBNER, REINHARD
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(202) 371-2540
                                                                                                                                                                                                                                                                                                                                                                       253.00
4.961
100.000
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100.000
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-09-030-607-209
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seq_documentation_block:
; Sequence 209, Application US/09439313
                                                                  seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-439-313-209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FER-1000
CLASSIFTONE: 25-FER-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-09-030-607-209 from: 1
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Patent No. 6262245
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21/
TELECOMMUNICATION INFORMATION:
TELECHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Xu, Jiangchun .
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUN
NUMBER OF SEQUENCES: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                153
                                                                                                                                                                                                       103 CTGGAGCCAAAAAGGACACAAAGGACTCTCGACCCAAACTGCCCCAGACC 152
                                                                                                                                                                                                                           58 roGlyAlaLysLysAspThrLysAspSerArgProLysLeuProGlnThr 74
                                                                                                                                                                                                                                                                                         53 GCTCCTTGTGGCCCTCTCCTACACTCTGGCCAGAGATACCACAGTCAAAC 102
                                                                                                                                                                                                                                                                                                                41 uLeuLeuValAlaLeuSerTyrThrLeuAlaArgAspThrThrValLysP
                                                                                                                                                                                                                                                                                                                                                                                                       25 ValArgLysSerArgValAlaMetGluLysIleProValSerAlaPheLe
                                                                                                                                                         75 LeuSer 76
                                                                                                                                                                                                                                                                                                                                                                                3 GTGAGGAAATCCAGAGTTGCCATGGAGAAAATTCCAGTGTCAGCATTCTT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 159 base pairs
                                                                                                                CTCTCC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seattle
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4.846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210121.427C3
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; TYPE: DNA; ORGANISM: Homo sapien US-09-439-313-209
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US-09-674-266A-181 x US-09-439-313-209
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                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-916-576B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-09-439-313-209 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 209
LENGTH: 159
                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                              Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SOlk, John
APPLICANT: Day, Craig
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Xu, Jiangchun
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                                                                                                            APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                              APPLICANT: YU, GUO-LIANG
APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
COMPUTER
                                                                                                                                                                                                                                                                                                                                                                                                                153 CTCTCC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 CTGGAGCCAAAAAGGACACAAAGGACTCTCGACCCAAACTGCCCCAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 roGlyAlaLysLysAspThrLysAspSerArgProLysLeuProGlnThr 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 LeuSer 76
                  COUNTRY: US
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GTGAGGAAATCCAGAGTTGCCATGGAGAAAATTCCAGTGTCAGCATTCTT
                                                                                              STREET:
                                                                                         ADDRESSEE: STERNE, KESSLER, GOLDSTEI
STREET: 1100 NEW YORK AVENUE, SUITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTCCTTGTGGCCCTCTCCTACACTCTGGCCAGAGATACCACAGTCAAAC
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                                                                       WASHINGTON
                                                                                                                                                                                                                                                                                            , Application US/08916576B 6171816
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Fanger, Gary
Retter, Mark
READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
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Reed, Steven G.
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4.846
100.000
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                                                                                                                  KESSLER, GOLDSTEIN & FOX, P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
Percent Identity:
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alignment_block: us-09-674-266A-181 \times us-08-916-576B-3
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US-08-916-576B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-08-916-576B-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 60/024,347
APPLICATION NUMBER: US 60/024,347
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 141
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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145 ThrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMetPh
                                                                                            130 ysLeuAlaGluGlnPheValLeuLeuAsnLeu.....ValTyrGluThr 144
                                                                                                                                  288 AGCTTGCAAAGCTCTAAAGCCCAAATTTGCAGAATCTACGGAAATTTCAG
                                                                                                                                                                                                                                                                                    191 GAGATCATATTCATTGG...AGGACACTGGAAGATGGGAAGAAAGAAGCA 237
                                                                                                                                                                                                                                                                                                                                                                141 GCTCCTCGTCATCTTCTGATGGACATAATGGGCTTGGAAAGGGTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                 97 LysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGluCysPr 113 :::|||::: ||| ||| ::: |||
                                                                                                                                                                                                                                                                                                                          80 lyAspGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrLysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                           91 GAGACGCGGCCTCGTCTCGGGGCCACCTGTTTGCTGGGCTTCAGTTTCCT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 AspSerArgProLysLeuProGlnThr.....
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STRANDEDNESS: doub
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
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                                                         AACTCTCCCATAATTTTGTTATGGTAAATCTTGAGGATGAAGAGGAACCC
                                                                                                                                                                  OHISSERGINALALEULYSLYSVALPheAlaGluAsnLysGluIleGlnL 130
                                                                                                                                                                                                           GCTGCCAGTGGACTGCCCCTGATGGTGATTATTCATAAATCCTGGTGTGG
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9b_est2:BE737345
gb_est1:AW369331
gb_est2:BE73653
gb_est2:BE58540
gb_est2:BE565542
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gb_est2:BF680376
gb_est1:AL543432
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gb_est2:BE748141
gb_est2:BF733142
gb_est2:BG501149
gb_est2:BI770077
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Database length: -1841457050
Search time (sec): 1720.980000
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Query length:
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gb_est2:BM129777
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gb_est2:BI760685
                                                                                                                                                                                                                                                          gb_est2:BI763228
gb_est1:AA316115
                                                                                                                                                                                                                                                                                                               gb_est2:BM006784
gb_est2:BM006554
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gb_est2:BM006510
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gb_est2:BE870718
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                                                                                                                             gb_est2:BE867131
                                                                                                                                         gb_est2:BF207999
                                                                                                                                                       gb_est2:BF680021
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-DB-EST -QFMT-fastap -SUFFIX-p2n.rst -GAPOP=12.000 -GAPEXT-4.000
-MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT=0.000 -GAPEXT-0.000
-QGAPEXT-0.050 -XGAPOP=10.000 -XGAPEXT-0.050 -FGAPOP-6.000
-FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000
-DELEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000
-DELEXT-7.000 -START-1 -MATRIX-blosum62 -TRANS-human40.cdi
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-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -HEAPSIZE-500
-MINLEN-0 -MAXLEN-200000000 -USER-US09674266_eCGN1_1_2564
-NCPU-6 -TCPU-3 -LONGLOG -DEV_TIMEOUT-120 -WARN_TIMEOUT-30
-NO_XLPXY -WAIT -THREADS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MODEL=frame+
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p2n.model -DEV=xlh
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1760.49
1752.07
1736.57
1738.66
1728.64
1702.30
1702.30
1703.94
1680.49
1676.77
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                                                     2.4e-88
1.8e-87
1.3e-87
6.5e-87
1.4e-85
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.3e-102
.2e-101
.6e-99
.0e-99
.9e-99
.9e-99
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.8e-96
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 version 4.5
                                   BF733142 EST039 HUMAN hepatocel BG501149 602546389F1 NIH_MGC_60 B177007 603053412F1 NIH_MGC_12 AW956284 EST368354 MAGE reseque BG285246 602409569F1 NIH_MGC_12 BM12977 1f23a808.y1 Melton Norm BE796856 601588166F1 NIH_MGC_11 BM12977 1f23a808.y1 Melton Norm BE796856 603615816F1 NIH_MGC_11 BM006510 60361541F1 NIH_MGC_11 BM006554 60361521F1 NIH_MGC_11 BM006554 60361521F1 NIH_MGC_11 BM006658 603615373F1 NIH_MGC_11 BM006658 603615373F1 NIH_MGC_11 BM006669 603615373F1 NIH_MGC_11 BM006669 603615373F1 NIH_MGC_11 BM006554 60215473787 NIH_MGC_15 BG823844 602729503F1 NIH_MGC_15 BG823844 602729503F1 NIH_MGC_15 BF680037 EST178713 COlon carcin BF680376 602154740F1 NIH_MGC_15 BF680376 F1 ST178713 COlon carcin BF680376 602154740F1 NIH_MGC_15 BF680775 603154749F1 NIH_MGC_15 BF780718 6031642973F1 NIH_MGC_15 B170027 603055968F1 NIH_MGC_15 B170027 603055968F1 NIH_MGC_15 B1700685 6031044871F1 NIH_MGC_15 B170685 6031044871F1 NIH_MGC_39 AW369331 QV1-BN0002-061299-039 AW369331 QV1-BN0002-061299-039 AW369331 QV1-BN0002-061299-039 AW369331 CONTENDORS NIH MGC_3
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SOURCE
ORGANISM
                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
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                                                                                                                             alignment_block:
                                                                                                                                                                                                 alignment_scores:
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                                                                                                                                                       Quality: 1008.00
Ratio: 5.169
Percent Similarity: 100.000
                                                                                                              US-09-674-266A-181 x BG778248
                                                                                  Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                            12
                                                        12
                                            GlyProHisProSerArgArgLeuThrGlnGlyArgTrpValArgLysSe
rArgValAlaMetGluLysIleProValSerAlaPheLeuLeuLeuValA
                            GGACCGCATCCTAGCCGCCGACTCACACAAGGCAGGTGGGGTGAGGAAATC
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BG778248 from: 1

to: 666

61

Percent Identity: 100.000

Length:

195 0

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gb_est2:BG172599
gb_est2:BF801670
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LOCUS BG778248
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gb_htc:AK007677
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 666)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
BG778248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG778248.1 GI:14048565
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       205
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/lab_host="DH10B (T1 phage-resistant)"
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/note="Organ: prostate; Vector: pDNR-LIB (Glontech);
/note="Organ: prostate; Vector: pDNR-LIB (Glontech);
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/note="Organ: prostate; Site_2: Sit1 (ggccattatggcc);
/note="Organ: prostate; Site_2: Sit1 (ggccattatggcc);
/note="Organ: politic graphs (ggccattatggccattatggcc);
/note="Organ: politic ggccattatggcc];
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/clone_lib="NIH_MGC_60"
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/db_xref="taxon:9606"
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19 602337015F1 NCI_CGA
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                            gb_est1:AW582256
                     Tel: +55-11-2707001
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?tl=QV4st2=QV4-ST0212-
120100-075-e10&t3=2000-01-12&t4=1)
                                                                                                                                               Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                           HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                              TCGTCTCTATGCTTACGAACCTGCAGATACAGCTCTGTTGCTTGACAACA
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/clone_lib="ST0212"
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                                                                                                                                                                                                                                                                                                                                                    Quality: 1002.00
Ratio: 5.165
Percent Similarity: 100.000
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AGTTGCCATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCCC
                                                                                                        gValAlaMetGluLysIleProValSerAlaPheLeuLeuLeuLeuValAlaL 46
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (1999)
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Plate: LLAM11504 row: h column: 04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-*Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: ECORV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dr primed and directionally cloned (BcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NHH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5201331"
/clone_lib="NIH_MGC_122"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B"
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sapiens cDNA clone IMAGE:5201331 5',
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LOCUS BG179160
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ORGANISM
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                                                                                                                                                                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM10186 row: o column: 08 High quality sequence stop: 732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BG179160
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EST.
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                                                                                                                                                                                                                                           quality sequence stop:
Location/Qualifiers
/clone="IMAGE:4431583"
/clone_lib="NIH_MGC_91"
/tissue_type="adenocarcinoma, cell'
/lab_host="DH10B (phage-resistant)"
                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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seq_documentation_block:
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Ratio: 5.147
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                                                                                                                                                                                                                                                                                                                              laLeuLysLeuLeuLysThrGlu 205
                                                                                                                                                                        rAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysA 198
                                                                                                                                                                                                                               SerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeuTy 181
                                                                                                                                                                                                                                                                                      LysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGlyAs
                                                                                                                                                          TGCTTACGAACCTGCAGATACAGCTCTGTTGCTTGACAACATGAAGAAAG
                                                                                                                                                                                                                TCTCTGACAGTTAGAGCCGATATCACTGGAAGATATTCAAATCGTCTCTA
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                                                                    gb_est2:BE748141
              601571509F1 NIH_MGC_55 Homo sapiens
mRNA sequence
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Note: this is a NIH_MGC Library."

174 c 158 g 183 t 1 others
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KEYWORDS
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US-09-674-266A-181 x BE748141
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BE748141.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 689)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="NIH_MGC_55"
/clone_lib="NIH_MGC_55"
/tissue_type="from acute myelogenous leukemia"
/lab_host="DH10B (TI phage-resistant)"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattaggcc)
Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattaggcc)
; Double-stranded cDNR was prepared from cell line RNA.
5; and 3; adaptors were used in cloning as follows: 5;
adaptor sequence: 5'-CACGGCCATATGGCC-3' and 3' adaptor
sequence: 5'-ATTCAAAGGCCGACGGCCGACATC-dT(30)BN-3'
(where B = A, C, Or G and N = A, C, G, Or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 14/15 colonies .
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

109 a 170 c 148 g 162 t
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      255 bp mRNA linear EST039 Human hepatocellular carcinoma subtracted c sapiens cDNA clone P39 5', mRNA sequence.
                                                                                                                                                                                                                       Email: wuling_z@hotmail.com
Human hepatocellular carcinoma cDNA research supported by Institute
of Digestive Disease, Henan Medical University; cDNA insert
sequencing: Genetech Biotechnology Company Limited. cDNA library
construction: Department of Nucleic Acid Research, Institute of
                                                                                                                                                                                                                                                                                                                     2 Jingba Road, Zhengzhou, 450003, Henan Province, Tel: 86 0371 3921444
Fax: 86 0371 6960571
                                                                                                                                                                                                                                                                                                                                                               Contact: Wuling Zhu
Department of Nucleic Acid Research
Institute of Digestive Disease
2 Jingba Road, Zhengzhou, 450003, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhu,W., Duan,F., Liu,D., Ma,J., Bai,J. and Gao,T. Suppression subtracted hybridization to identify differentially expressed genes of hepatocellular carcinoma and expressed sequences.
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1 (bases 1 to 755)
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                                                                                                                                                                                     primer:
                 237
                                                                     /organism="Homo sapiens"
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/clone="p39"
/clone_lib="Human hepatocellular
                               /note="Organ:
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                                                     ibrary
           Liver"
158 g
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US-09-674-266A-181 x BF733142
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 740)
                                      Homo sapiens
                                                                                              mRNA sequence.
BG501149
                                                                                                                        602546389F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4668575
                                                                     EST
                                                                                  BG501149.1 GI:13462666
                                                                                                                                       BG501149
                                                       numan
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alignment_block:
US-09-674-266A-181 x BG501149
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TITLE
JOURNAL
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                                                                                                                                                                                                                                          LysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgG1 78
CysProHisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIl 128
                                                 ysSerLysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGlu 111
                                                                                                     TTGGGGTGACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATA 263
                                                                                                                      yTrpGlyAspGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrL 95
                                                                                                                                                                        AAGGACACAAAGGACTCTCGACCCAAACTGCCCCAGACCCTCTCCAGAGG
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Ratio:
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (where B - A, C, or G and N - A, C, G, or T). Average insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           979.00
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171 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 788)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                    248
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Location/Qualifiers
           /notes "Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                               /organism="Homo saplens"
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/clone="IMAGE:5202866"
/clone_lib="NIH_MGC_122"
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alignment\_scores:

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VERSION
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LOCUS AW956284
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 721)

Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Hol, L., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
                                                                                       EST.
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spLysHisLeuSerProAspGlyGlnTyrValProArgIleMetPheVal 162
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Plate: 90
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/db_xref="taxon:9606"
/clone_lib="MAGE resequences, |
/note="Vector: pBluescriptSKm"
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REFERENCE
AUTHORS
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Percent Similarity:
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                                                                                                                                                        14 HisProSer...ArgArgLeuThrGlnGlyArgTrpValArgLysSerAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.

Email: ggapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10467 row: i column: 18
High quality sequence stop: 750.
Location/Qualifiers

1 0462
                euSerTyrThrLeuAlaArgAspThrThrValLysProGlyAlaLysLys 62
                                                                                     gValAlaMetGluLysIleProValSerAlaPheLeuLeuLeuLeuValAlaL 46
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TCTCCTACACTCTGGCCAGAGATACCACAGTCAAACCTGGAGCCAAAAAG
                                                                   AGTTGCCATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCCC
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1 (bases 1 to 866)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: No
Site_2: Sall; Cloned unidirectionally; Oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies
Note: this is a NIH_MGC Library."

a 194 c 189 g 212 t 1 others
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/clone="IMAGE:4539353"
/clone_lib="NIH_MGC_91"
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seq_name: gb_est2:BM129777
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1 (bases 1 to 581)

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,

Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,

Hillier,L., Marra,M., Pape,D., Wylle,T., Martin,J., Blistain,A.,

Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.,

Jackson,Y. and Bowers,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BM129777 581 bp mRNA linear EST 27-NOV-2: if23a08.yl Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens CDNA 5' similar to TR:095994 095994 SECRETED CEMENT GLAND PROTEI
                 Library was constructed by Dr. Douglas Melton DNA: Washington University Genome Sequencing Center For obtaining a clone please contact: Juliana Brown
                                                                                                                                  Tel: 617-495-1812
Fax: 617-495-8557
                                                                                                                                                                                        MA 02138
                                                                                                                                                                                                                Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity
                                                                                                                                                                                                                                                                                              Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi
                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Other_ESTs: if23a08.x1
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                                                                                                        Email: dmelton@biohp.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                       Endocrine Pancreas Consortium
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(brown@fas.harvard.edu)
                                                    Douglas Melton DNA sequencing by equencing Center For information
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/sex="Both"
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140 c
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/dev_stage="Adult"
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5.138
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Tissue Procurement: DCTD/DTP
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab_host="DHIOB" (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
a 225 c 207 g 220 t
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/clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
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                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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                                                             CysProHisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIl 128
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/lab_host="DH10B (Ti phage-resistant)"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
/note="Organ: prostate; Vector: pDNR-LIB (ggcgattatggcc);
site_1: SfiI (ggcgcattatggcc); Site_2: SfiI (ggcattatggcc);
site_1: SfiI (ggcgcattatggcc); Site_2: SfiI (ggcattatggcc);
pouble-stranded cDNA was prepared from cell line RNA.

5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ATTCTAGAGGCGACTTATTGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCGGACATG-GT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_60"
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US-09-674-266A-181 x BE870718
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Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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163 c 156 g
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/db_xref="taxon:9606"
/clone="IMAGE:3852448"
/clone_lib="NIH_MGC_65"
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                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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http://image.llnl.gov
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/clone="IMAGE:5421109"
/tissue_type="ductal carcinoma,
                     /clone_lib="NIH_MGC_110"
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197 ysAlaLeuLysLeuLeuLysThrGluLeu 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 erTyrThrLeuAlaArgAspThrThrValLysProGlyAlaLysLysAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 TGCCATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 lAlaMetGluLysIleProValSerAlaPheLeuLeuLeuValAlaLeuS
                                                                                                                                                                                             ysHisLeuSerProAspGlyGlnTyrValProArgIleMetPheValAsp 163
                                                                                                             CCATCTCTGACAGTTAGAGCCGATATCACTGGAAGATATTCAAACCGTCT 485
                                                                                                                                                                              ACAAAGGACTCTCGACCCAAACTGCCCCAGACCCTCTCCAGAGGTTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTACACTCTGGCCAGAGATACCACAGTCAAACCTGGAGCCAAAAAGGAC
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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5.070
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9b_pat:AX231601
9b_pat:AR007791
9b_pat:AR177367
9b_pat:AX314953
9b_pat:AX314953
9b_pat:AX341524
9b_pat:AX341524
9b_pat:AX341524
9b_pat:AX341388
9b_pat:AX3413857
9b_pat:AX34113857
9b_pat:AX341136194
9b_pat:AX341213
9b_pat:AX341229
9b_pat:AX341229
9b_pat:AX3241229
9b_pat:AX322727
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9b_pat:AX32273
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WARN:
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Database length: 1873333701
Search time (sec): 1915.830000
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gb_pat:AX011612
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gb_pat:AX341084
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gb_pr:AF088867
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-DB=GenEmb1 -QEMT=fastap -SUFFIX=011p2n.rge -GAPOP=4.500
-GAPEXT=0.050 -MINMATCH=0.100 -LOOPEXT=0.000
-QAAPOP=4.500 -QGAPEXT=0.050 -YGAPOP=60.000 -XGAPEXT=60.000
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
-DELOP=6.000 -DELEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
-DELOP=6.000 -DELEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
-THR_MIN-1 -ALIGN=15 -MODE-LOCAL -OUTEMT=pfs -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09674266_@CGN1_1_3973 -NCPU=6 -ICPU=3 -LONGLOG
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Copyright (c)
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3712.56

3712.51

3709.14

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3406.20

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2.5e-211
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3.1e-198
3.1e-197
1.9e-197
1.9e-197
1.6e-181
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1.6e-181
1.6e-181
     2. 4e-133
2. 4e-120
2. 9e-119
3. 1e-1119
3. 3e-105
1. 9e-105
1. 9e-105
3. 1e-101
3. 1e-101
3. 6e-100
3. 6e-100
3. 6e-99
5. 6e-99
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RECO15503 Homo sapiens, anterior
ARI123828 Sequence 1 from patent
AX341084 Sequence 7 from patent
AX341084 Sequence 7 from patent
AX341084 Sequence 7 from patent
AX231601 Sequence 61 from patent
AX341234 Sequence 1481 from patent
AX341234 Sequence 215 from patent
AX341234 Sequence 215 from patent
AX341234 Sequence 215 from patent
AX341236 Sequence 2131 from patent
AX341236 Sequence 133 from patent
AX341236 Sequence 915 from patent
AX341236 Sequence 915 from patent
AX341238 Sequence 915 from patent
AX341238 Sequence 2131 from patent
AX341238 Sequence 216 from patent
AX341237 Sequence 217 from patent
AX341239 Sequence 1346 from patent
AX341239 Sequence 1476 from patent
AX341239 Sequence 32 from patent
AX341239 Sequence 32 from patent
AX341239 Sequence 32 from patent
AX341230 Sequence 32 from patent
AX341240 Sequence 32 from patent
AX34125 Sequence 32 from patent
AX34125 Sequence 32 from patent
AX34126 Sequence 1363 from patent
AX341216 Sequence 136 from patent
AX341216 Sequence 136 from patent
AX341116 Sequence 1370 from patent
AX341116 Sequence 1380 f
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AX015056 Sequence 265 from Pa
AF088867 Homo sapiens putative
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gb_pat: AX106428
gb_pat: AX140719
gb_pat: AX200579
gb_pat: AX267235
gb_pat: AR123859
gb_pat: AX062783
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KEYWORDS
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
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seq_documentation_block:
LOCUS AX011612
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                                                                                                                                                                                                                                             ysIleProValSerAlaPheLeuLeuLeuValAlaLeuSerTyrThrLeu
                                                                                                                      AlaArgAspThrThrValLysProGlyAlaLysLysAspThrLysAspSe
|||||||||||||||||||||||||||
GCCAGAGATACCACAGTCAAACCTGGAGCCAAAAAGGACACAAAGGACTC
                                                                                                                                                                                                      LysProLeuMetIleIleHisHisLeuAspGluCysProHisSerGlnAl
                                                                            AAACCCTTGATGATTATTCATCACTTGGATGAGTGCCCACACAGTCAAGC
                                                                                                                                                               AAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCCCTCTCCTACACTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb_pat:AX011612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human nucleic acid sequences obtained Patent: WO 9955858-A 8 04-NOV-1999; SCHMITT ARMIN (DE); SPECHT THOMAS (DE)
                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8 from AX011612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL E BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES (DE); PILARSKY CHRISTIAN (DE)
LOCATION/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pilarsky,C
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/db_xref="taxon:9606"
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 Sequence 265 from Patent W09953040.
AX015056
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SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN (DE); PILARSKY CHRISTIAN (DE)
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LOCUS AF088867
DEFINITION Homo sapiens
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Zhang, J.S. and Smith, D.I.
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Zhang, J.S. and Smith,
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/product="putative secreted
/protein_id="AAF22484.1"
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                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                  Direct Submission
Submitted (30-AUG-1998) Pathology and Lab.
200 SW 1st St., Rochester, MN 55905, USA
Location/Qualifiers
          /note="differentially expressed in tumors; similar
Xenopus cement gland-specific secreted protein"
/codon_start=1
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LOCUS AF038451
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US-09-674-266A-181 x AF088867
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mRNA, complete cds
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           PRI 03-DEC-1998 nolog (hAG-2/R)
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euSerTyrThrLeuAlaArgAspThrThrValLysProGlyAlaLysLys
                                                                                                                                                              gValAlaMetGluLysIleProValSerAlaPheLeuLeuLeuValAlaL
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                                                                                                                                             AGTTGCCATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCC
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Submitted (09-DEC-1997) Surgery,
Road, MSLS Building, Room P228,
Location/Qualifiers
1. 1077
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                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thompson, D.A
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AF038451.1 GI:3779225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="secreted cement gland protein xAG-2 homolog"
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/note="isolated from estrogen receptor-positive breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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Submitted (21-DEC-1998) Laboratory of Medicine and Pathology, Mayo
Clinic, 200 SW 1st Street, Rochester, MN 55905, USA
Location/Qualifiers
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Zhang, J.S. and Smith, D.I.
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/db_xref="taxon:9606"
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                                                                                                                                                                             AGAAAGCTCTCAAGTTGCTGAAGACTGAATTG
                                                                                                                                                                                                                             TCTCTATGCTTACGAACCTGCAGATACAGCTCTGTTGCTTGACAACATGA
                                                                                                                                                  gb_pr:BC015503
                                                       Homo sapiens, anterior gradient 2 (Xenepus MGC:9112 IMAGE:3852448, mRNA, complete cds. BC015503 BC015503.1 GI:15930124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                       Homo sapiens
                                      human.
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US-09-674-266A-181 x BC015503
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erTyrThrLeuAlaArgAspThrThrValLysProGlyAlaLysLysAsp 63
                                                                                                                                                                                                          lAlaMetGluLysIleProValSerAlaPheLeuLeuLeuValAlaLeuS 47
                                                                                           CCTACACTCTGGCCAGAGATACCACAGTCAAACCTGGAGCCAAAAAGGAC
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                                                                                                                                                                                   TGCCATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCCCTCT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 20 Row: o Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6652811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
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/protein_id="AAH15503.1"
/db_xref="GI:15930125"
/translation="meKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTL
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QFVLLNLVYETTDKHLSPDGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALL
LDNMKALKLLKTEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="LocusID:10551"
/db_xref="taxon:9606"
/clone="MGC:9112 IMAGE:3852448"
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/clone_lib="NIH_MGC_65"
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alignment_block:
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              31 aMetGluLysIleProValSerAlaPheLeuLeuLeuValAlaLeuSerT 48
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Human XAG-1 polynucleotides and pol
Patent: US 6171816-A 1 09-JAN-2001;
                                                                                                                                                                                                      Quality:
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Quality:
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LOCUS AX341084
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Sequence 1331 from Patent W00196388.
AX341084.1 GI:18137066
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS
TITLE
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VERSION
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                                             FEATURES
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G
                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 543)

Boyd.R.S., Stamps,A.C., Terrett,J.A. and Tyson,K.L.

Bcmp-7 as marker for diagnosis of breast cancer

Patent: WO 0163290-A 7 30-AUG-2001;

Oxford GlycoSciences (UK) Limited (GB)

Location/Qualifiers

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AX231601
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alignment_block:
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                                                        79 TrpGlyAspGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrLy
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                                                                                                                           ysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGly
sSerLysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGluC 112
                                     TGGGGTGACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-JUN-1997) Surgery, Stanford, 1201 Building, Room P228, Stanford, CA 94305, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="hAG-2/C"
/note="similar to Homo sapiens protein hAG-2/R deposited in GenBank Accession Number AF038451, and to Xenopus laevis cement gland proteins np77 deposited in GenBank Accession Number U82110 and XAG-2 deposited in GenBank Accession Number AF025474"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="secreted cement gland protein XAG-2 homolog"
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/db_xref="GI:3779197"
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/tissue type="adenocarcinoma"
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/db_xref="taxon:9606"
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alignment_block:
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                                   GlnLysLeuAlaGluGlnPheValLeuLeuAsnLeuValTyrGluThrTh 145
TrpGlyAspGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrLy
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AR177367
AR177367.1 GI:17919722
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Edwards, J.-B. Dumas Milne., Duclert, A.
Complementary DNAs
Patent: US 6312922-A 61 06-NOV-2001;
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  CCTCTCCTACACTCTGGCCAGAGATACCACAGTCAAACCTGGAGCCAAAA
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AX341234
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/db_xref="taxon:9606"
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129 GlnLysLeuAlaGluGlnPheValLeuLeuAsnLeuValTyrGluThrTh 145
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                                               ArgValAlaMetGluLysIleProValSerAlaPheLeuLeuLeuValAl
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                                    AGAGTTGCCATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Sequence 2200 from Patent WO0196388
AX341953
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                   Sequence 215 from Patent Ax351468
                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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AX067336
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Quality:
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                                                                                                                                                            cancer
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Database sequences: 1736436
Database length: 858457221
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                                                                        This invention describes novel polypeptides and their encoding nucleic acids derived from human pancreatic tumor tissue which have cytostatic activity. The sequences are also useful in producing pharmaceutical compositions for treatment of pancreatic tumors. AAZ52858-Z53014 represent expressed sequence tag (EST) fragments derived from a human pancreatic tumor cDNA library and which encode the proteins represented in AAY73814-Y74252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human nucleic acid sequences from proteins -
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                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                             comprising secretory signal nucleotide sequence
   97WO-JP03239
                                                                                        Location/Qualifiers
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                                                                   "human protein signal"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a secretory signal isolated from stomach cancer cells. Its protein can be used as nutritional sources or supplements. The proteins also have cytokine functions, immune modulating functions, haematopoissis regulating activity, activin/inhibin regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity.
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(SAGA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human proteins with
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                                                                                                                                                                                       78
                                                                           hrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMetPhe
                                 LysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGl
                                                                                                                                ysSerLysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGlu
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DB; AAW37872.
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SAGAMI CHEM RI
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02-JUN-1999
23-JUN-1999
07-JUL-1999
26-JUL-1999
30-NOV-1999
20-DEC-1999
                                                                           The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO531 PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, PRO1005, PRO1007, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1187, PRO1187, PRO1281, PRO33, PRO39, PRO834, PRO1317, PRO1710, PRO2094, PRO2145 OR PRO2198, PRO antagonists can be used to inhibit tumour cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosuppressive; immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; angiogenic; hypothalamic disorder; plandular disorder; macrophagal disorder; plandular disorder; blastocoelic disorder; epithelial disorder; stromal disorder; blastocoelic disorder;
growth. The PRO polypeptides and nucleotides are useful in the treatment, diagnosis and prevention of cancer. The antibodies and other anti-tumour compounds maybe used to treat various conditions, including
                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                       Thirty PRO
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Watanabe CK,
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b; AAB24070.
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99WO-US12252.
99WS-0141037.
99US-0143048.
99US-0145698.
99WO-US28313.
99WO-US30911.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         those characterised by overexpression and/or activation of the amplified PRO genes. Exemplary conditions or disorders to be treated with such antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR primers and hybridisation probes used in the isolation of the human PRO sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human PRO polynucleotide and protein sequences given in the exemplification of the human protein report invention.
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etLysLysAlaLeuLysLeuLeuLysThrGluLeu 206

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seq_documentation_block:
ID AAH35026 standard; cl
XC AAH35026;
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XX O3-SEP-2001 (first e
XX Human; colon cancer ar
XX Human; colon cancer;
KW Human; colon cancer;
KW Human; colon cancer;
KW Colorectal carcinoma;
XX Homo sapiens.
XX Homo sapiens.
XX PAR-2001.
XX O5-APR-2001.
XX O5-APR-2001.
XX PPR 29-SEP-1999; 99US-C
XX O3-NOV-1999; 99US-C
XX Ruben SM, Barash SC,
XX Ruben SM, Barash SC,
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                                                                                                                                                                 Percent Similarity:
Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated P, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB7789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                       N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
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P-PSDB; AAG75621.
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAZ77486
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AAZ77486 standard;
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                     09-APR-1998;
                                                                                                                     Homo sapiens.
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                                                                                                                                                         Expressed sequence tag; EST; human; ovarian tumor;
                                                                                                                                                                                  Human ovarian tumor cDNA library derived EST
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                                             09-APR-1998;
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nLysLeuAlaGluGlnPheValLeuLeuAsnLeuValTyrGluThrThrA 146
                                                                          ProHisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleGl 129
                                                                                                                                                                                                                                      GGGTGACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAAAT
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                                               CCACACAGTCAAGCTTTAAAGAAAGTGTTTGCTGAAAATAAAGAAATCCA
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                                                                                   New isolated human XAG growth factor(s) - used to for treating e.g. liver, lung or breast diseases hyperproliferative disorders, e.g. cancer.
                                                                                                                                            Dillon PJ,
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                                                                                                                                                                                                                                                                                                                        emphysema;
                                                                                                                                                                                                                                                                                                                                                       Human XAG growth factor huXAG-1 cDNA
                                                                    Claim 5; Fig 1; 141pp; English.
                                                                                                                            WPI; 1998-169093/15
                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                           23-AUG-1996;
                                                                                                                                                                                           22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                         HuxAG-1; XAG;
                                                                                                                                                                                                                                                                                                                                                                        28-AUG-1998
                                                                                                                   P-PSDB; AAW37844.
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                                                                                                                                                                                                                                                                                                                                 tumour marker;
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                                                                                                                                                                                                                                                                                                                               growth factor; colon cancer-specific gene;
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71..130
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This cDNA clone codes for huxAG-1 (see AAM37844), a member of a novel family of human growth factors also including huxAG-2 (see AAM37845) and huxAG-3 (see AAM37845). These proteins share homology with the XAG protein of Xenopus laevis, which is involved in embryogenesis and is expressed in adult tissue. Expression of huXAG-1 has been discovered in colon cancer tissue, with no corresponding expression in healthy colon tissue. The huXAG-1 gene, also designated colon cancer-specific gene (CCSG), provides a molecular marker for

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US-09-674-266A-181 x AAV19155
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to:
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                                                                                     uAlaGluGlnPheValLeuLeuAsnLeuValTyrGluThrThrAspLysH
                                                                                                                                                                                                         SerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleGlnLysLe 131
                                                                                                                                                                                                                                                                                                                             hrSerAsnLysProLeuMetIleIleHisHisLeuAspGluCysProHis
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isLeuSerProAspGlyGlnTyrValProArgIleMetPheValAspPro
                                                                                                                                                                             AGTCAAGCTTTAAAGAAAGTGTTTGCTGAAAATAAAGAAATCCAGAAATT
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seq_documentation_block:
ID AAF63314 standard; cE
XX AAF63314;

AC AAF63314;

XX AAF63314;

XX DT 04-MAY-2001 (first e
XX Human huXAG-1/CCSG cc
XX Human pointeration; l
KW cell proliferation; l
KW hepatitis; cancer; cc
CX SHOMO sapiens.

XX US6171816-B1.

XX US6171816-B1.

XX US6171816-B1.

XX 22-AUG-1997; 97US-(
XX 23-AUG-1996; 96US-(
XX 23-AUG-1997; 97US-(
XX 23-AUG-1997; 97US-(
XX PPR 23-AUG-1997; 97US-(
PR 27-AUG-1997; 97US-(
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                                                                                                                                                  This invention relates to a human growth factor polypeptide huXAG-1 also CC known as a colon cancer specific gene (CCSG). HuXAG-1 stimulates cell CC proliferation as a growth factor. The HuXAG-1 protein is useful for cidentifying compounds capable of enhancing or inhibiting cellular response induced by huXAG-1. The protein is also useful for stimulating CC proliferation of cells e.g. colon, breast, liver and lung cells, and the pathologies such as fulminant liver failure caused by cirrhosis, liver canage caused by viral hepatitis and toxic substances, for preventing and CC damage caused by viral hepatitis and toxic substances, for preventing and CC cancer. HuXAG-1 and the identified antagonist are useful for treating cancer in particular colon cancer. Detecting altered levels of huXAG-1 cancers. The gene encoding huXAG-1 is useful for monitoring human colon cancer in useful for monitoring human colon cancer. HuXAG-1 carcinoma. huXAG-1 is useful for monitoring human colon cancer in huXAG-1 carcinoma. huXAG-1 is useful for monitoring human colon cancer in huXAG-1 carcinoma. huXAG-1 is useful for monitoring human colon cancer in huXAG-1 carcinoma. huXAG-1 nucleic acid molecules are also useful for charges cancer in huXAG-1 carcinoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human growth factor polypeptide useful for diagnosing and treating colon cancer and liver diseases, to prevent and heal damage to the lungs and for identifying modulators of therapeutic use -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-136872/14.
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                                                                                                                              chromosome identification. The
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                                                                                                                              present sequence
                                                                                                                                      represents cDNA encoding
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seq_documentation_block:
ID AAV59320 standard; cl
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AC AAV59320;
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DT 21-DEC-1998 (first e
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Nucleotide sequence e
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KW ss; human; mucous-mec
KW bacterial colonisatic
KW chronic obstructive p
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US-09-674-266A-181 x AAF63314
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                                                                                                                                                                                           seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV59320
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                                                                                                                                                                                                                                                                                                                                                                                                                                  148
ss; human; mucous-mediated function; adhesion; tumour metastasis;
bacterial colonisation; microbial infection; AIDS; cystic fibrosis;
chronic obstructive pulmonary disease; asthma; Crohn's disease;
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                                                          Nucleotide sequence encoding zsig10 polypeptide.
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Ratio: 1.000
Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uAlaGluGlnPheValLeuLeuAsnLeuValTyrGluThrThrAspLysH 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGlyAs 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yrThrLeuAlaArgAspThrThrValLysProGlyAlaLysLysAspThr
                                                                                                                                                                                                                                                                                                                                                             SerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeuTy 181
                                                                                                                                                                                                                                                                                                                                                                                                                    isLeuSerProAspGlyGlnTyrValProArgIleMetPheValAspPro 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGGACTCTCGACCCAAACTGCCCCAGACCCTCTCCAGAGGTTGGGGTGA
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alignment_block:
US-09-674-266A-181 x AAV59320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The human polypeptide zsigl0 is involved in mucous-mediated functions such as adhesion. The products of the invention can be used in the study and treatment of e.g. tumour metastasis, bacterial colonisation, susceptibility to and persistence of infection, microbial infections, AIDS, cystic fibrosis, chronic obstructive pulmonary disease, asthma, sinonasal inflammatory disease, inflammatory bowel disease, bronchitis, or Crohn's disease. The products can also be used for detection, diagnosis and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 37; Page 80-81; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated mucous-associated polypeptide, zsigl0 - used to develop products for treating e.g. tumour metastasis, microbial infections, cystic fibrosis, asthma, bronchitis or inflammatory bowel disease
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P-PSDB; AAW77365.
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                                                                                GACTCTCGACCCAAACTGCCCCAGACCCTCTCCAGAGGTTGGGGTGACCA
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erAsnLysProLeuMetIleIleHisHisLeuAspGluCysProHisSer
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                            ACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAAATCCAAGACAA
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seq_documentation_block:
ID AAS13480 standard; DN
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AC AAS13480;
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DT 19-DEC-2001 (first e
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DNA encoding breast c
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Breast cancer cell me
KW metastasis; cytostati
KW vaccine; chromosome 7
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Homo sapiens.
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Homo sapiens.
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FT mat_peptide 11...
FT mat_peptide 71...
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FT mat_peptide 71...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Breast cancer cell membrane protein 7; BCMP 7; breast cancer; metastasis; cytostatic.; gene therapy; antibody; antisense; vaccine; chromosome 7p21.3; ds.
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                                   Diagnosing, preventing and treating breast cancer using cell membrane protein BCMP 7 -
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Ratio: 1.000
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                 tLysLysAlaLeuLysLeuLeuLysThrGluLeu
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seq_documentation_block:
ID AAZ40803 standard;
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               alignment_block:
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                                                                                                                                                                          CC extended cDNAs (or genomic DNAs obtainable from them) may be used to CP prepare PCR primers and probes. These are useful for forensic matching or CC propartive identification by DNA sequencing. They may also be used in CC proteins encoded by the extended cDNAs are useful in identification of CC proteins encoded by the extended cDNAs are useful in identification of CC tissue types or cell species, as well as identifying tissue specific CC soluble proteins. The sequences can be used for chromosome mapping and CC identification of genes associated with hereditary diseases or drug CC response. Signal sequences from the cDNAs can be used in construction of Secretion vectors. Other sequences derived from the extended cDNAs can be used to clone upstream genomic DNA sequences including promoters. This is CC used to clone upstream genomic DNA sequences including promoters. This is considered that interact with promoter CC sequences. Some of the proteins may be useful in diagnosing and treating CC several disorders including, but not limited to: cancer, hyperlipidaemia, CC cardiovascular and neurodegenerative disorders, autoimmune diseases, and crheumatic diseases, embryogenic disorders, hypertension, renal injury, cC amino acidurias, hypoglycaemia, male rat infertility and myopathies.
                                             Ratio:
Percent Similarity:
US-09-674-266A-181
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10-AUG-1998;
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                                                                                                                                                                                                                                                                                                                              GAAGAAAGCTCTCAAGTTGCTGAAGACTGAATTG
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is the nucleotide sequence of the open reading frame of a novel human protein comprising a secretory signal (AAV29047), isolated from stomach cancer cells. Its proteins can be used as nutritional sources or supplements. The proteins may also have cytokine functions, immune modulating functions, haematopoiesis regulating activity, activiny/inhibin regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity.
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                                                                              AlaGluGlnPheValLeuLeuAsnLeuValTyrGluThrThrAspLysHi 148
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              GTCAAGCTTTAAAGAAAGTGTTTGCTGAAAATAAAGAAATCCAGAAATTG
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                                                                                                                                                                                                                                                    CAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAAATCCAAGAC
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GCAGAGCAGTTTGTCCTCCTCAATCTGGTTTATGAAACAACTGACAAACA
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seq_documentation_block:
ID AACOUILS standard; cD
XX AACOUILS;
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XX Human secreted protei
XX Human; 5' EST; expres
XX gene therapy: chromos
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XX O6-SEP-2000; 2000EP-C
XX D6-SEP-2000; 2000EP-C
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XX Homo sapiens.
XX Claim 1; SEQ ID 113;
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                                                                                                                                                                                              The present sequence is one of a large number of 5' ESTs derived from mRNAS encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAS or polyA+ RNAS derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-OT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
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therapy; chromosome
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                     Quality:
Ratio:
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                                                                                                                                      142 A;
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Percent Identity: 100.000
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Percent Similarity:

Align seg 1/1

to: AAC00115

from: 1

6 468 US-09-674-266A-181 x AAC00115

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seq_documentation_block:
ID AAF44884 standard;
                                                                                                                                                                                                                                                                                                                                                  seq_name:
                                                                                                                                                                                                                                                  Human breast cancer related protein coding sequence SEQ
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       New polynucleotides encoding breast tumor specific proteins, useful prevention, treatment and diagnosis of breast cancer - \,
                                                                                                        23-JUN-1999;
12-OCT-1999;
                                                                                                                                       23-JUN-2000; 2000WO-US17536
                                                                                                                                                                                  WO200078960-A2
                                                                                                                                                                                                                              Human; breast
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                                       WPI; 2001-041426/05.
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                                                                                   (CORI-) CORIXA CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                eGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeuValTyrGluThrT 145
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                                                            'n
                                                              Mitcham JL;
                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                             cancer; diagnosis; therapy; vaccine;
                                                                                                      99US-0140903
99US-0158980
                                                                                                                                                                                                                                                                                                                    cDNA;
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US-09-674-266A-181 x AAF44884
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Ratio: 1.000
Percent Similarity: 100.000
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AAA77903 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides the coding sequences for a number of breast cancer related proteins. These can be used in vaccinations against, diagnosis of and treatment of cancer, particularly breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; Page 132; 165pp; English
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                                                                                                                                                                                                                                                           170 aAspIleThrGlyArgTyrSerAsnArgLeuTyrAlaTyrGluProAlaA 187
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                                                                                                                                                                                                                                                                                                                    154
                                          Human colon tumour polypeptide; tumour
immunotherapy; diagnosis; progression;
                                                                            cDNA encoding human
                                                                                                   14-NOV-2000
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                                                                                                                                                                                                                                                                                             GlnTyrValProArgIleMetPheValAspProSerLeuThrValArgAl
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                                                                                                                                                                                                                                                                                                                                                    euLeuAsnLeuValTyrGluThrThrAspLysHisLeuSerProAspGly 153
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                                                                                                                                                                                                                                                                                                                                                                                       AGTGTTTGCTGAAAATAAAGAAATCCAGAAATTGGCAGAGCAGTTTGTCC
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                                                                                                                                              cDNA;
                                                                            colon tumour polypeptide,
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Gaps:
Percent Identity:
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                                                      antigen;
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                                                                            SEQ ID NO:183
                                                      cancer; vaccine;
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WO200037643-A2

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alignment_block:
US-09-674-266A-181 x AAA77903
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Comparison to the current result to previous results. The present sequence represents a cDNA encoding a human colon tumour
                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                       Align seg 1/1 to: AAA77903
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02-JUL-1999;
22-SEP-1999;
19-NOV-1999;
02-DEC-1999;
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                                                                  61
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                                                                                    rLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGlyA
                                                                                                                                                      TyrThrLeuAlaArgAspThrThrValLysProGlyAlaLysLysAspTh
               spGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrLysSerLys
                                                                                                                                     TACACTCTGGCCAGAGATACCACAGTCAAACCTGGAGCCAAAAAGGACAC
ACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAAATCCAAG
                                                                  AAAGGACTCTCGACCCAAACTGCCCCAGACCCTCTCCAGAGGTTGGGGTG
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, Yuqiu J;
                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                         Ratio:
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99US-0347496.
99US-0401064.
99US-0444242.
99US-0454150.
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Gaps: 0
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                                                                                                                                                                                                                                                                                                                                                                                            94 T; 0 other;
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAI28641
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The present invention describes colon tumour associated proteins (I) and the polynucleotides (II) that encode them. (I) have cytostatic activity. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of TCAPs by expressing inactive proteins or to supplement the patients own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host
                                                                                                                                                                                                                                                                                                                                           30-DEC-1999;
10-JAN-2000;
15-FEB-2000;
06-MAR-2000;
19-MAY-2000;
29-JUN-2000;
28-AUG-2000;
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                                                                                                                                                                                                                  Colon tumor
                                                                                                                                                                                                                                                                          King
                                                                                                                                                                                                                                                                                       Хu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; immunotherapy; diagnosis; colon cancer; colon tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Colon tumour related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAI28641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261
                                                                                                                                                                          Claim 25; Page 184; 472pp; English.
                                                                                                                                                                                                     prevention,
                                                                                                                                                                                                                                              WPI; 2001-441847/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-DEC-2000; 2000WO-US35596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunogenic;
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E, Wang T,
                                                                                                                                                                                                     associated proteins and nucleic acids useful for diagnosis and treatment of colonic cancer - \,
                                                                                                                                                                                                                                                                                                                                           2000US-0480321.
2000US-05194629.
2000US-0519444.
2000US-0575251.
2000US-0609448.
2000US-0649811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                          Secrist H,
Jiang Y;
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                                                                                                                                                                                                                                                                                        Benson
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                                                                                                                                                                                                                                                                                       Meagher MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer; ss
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alignment\_scores: Quality: 133.00 Ratio: 1.000 Percent Similarity: 100.000 alignment\_block: Align seg 1/1 to: AAI28641 from: 1 US-09-674-266A-181 x AAI28641 cell culturing the cell to express the protein. (II) and its complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (PCR) and hybridisation assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (I) may also be used as antigens in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity. Anti-(I) antibodies and antagonists may also be used to down regulate TCAP expression and activity. The anti-(I) antibodies may also be used as diagnostic agents for detecting the presence of TCAPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). Ant28460 to AAM24523 represent nucleotide and amino acid sequences given in the exemplification of the present invention. 361 164 311 148 261 131 211 114 161 111 Sequence 409 BP; 131 A; 104 C; 98 81 HisLeuSerProAspGlyGlnTyrValProArgIleMetPheValAspPr 164 euAlaGluGlnPheValLeuLeuAsnLeuValTyrGluThrThrAspLys 147 sSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleGlnLysL i31 TGGCAGAGCAGTTTGTCCTCCTCAATCTGGTTTATGAAACAACTGACAAA 310 CAGTCAAGCTTTAAAGAAAGTGTTTGCTGAAAATAAAGAAATCCAGAAAT 260 Length: 133
Gaps: 0
Percent Identity: 100.000 80 G; 94 T; 0 other; to: 409 360 60 64

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gb_est2:BM129777
gb_est1:AW956284
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gb_est2:BF747277
gb_est2:BF513917
gb_est1:AA316233
gb_est1:AA316233
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Database length: -1841457050
Search time (sec): 1725.590000
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gb_est2:BE870718
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gb_est1:AW582256
gb_est2:BI523582
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gb_est2:BI770077
gb_est1:AL543472
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gb_est2:BM006510
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gb_est2:BG386151
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-DB=EST -QFMT=fastap -SUFFIX=ollp2n.rst -GAPOP=4.500
-GAPEXT=0.050 -MINANCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GAPEXT=0.050 -MINANCH=0.100 -LOOPCL=0.000 -XGAPEXT=0.000
-GGAPEXT=0.050 -GAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
-FGAPOP=6.000 -DELEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
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-THR_MIN=1 -ALIGN=15 -MODE-LOCAL -OUTFMT=p5x -NORM=ext
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BM129777 1F23a08.y1 Melton Norm
AW956284 EST36354 MAGE reseque
BE796656 601588166F1 NIH_MGC_6
BE879718 601448570F1 NIH_MGC_6
BE285246 602409569F1 NIH_MGC_61
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AW369331
AA314225
AA437001
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AW582256
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29 EST187394 Colon carcin
70 QV3-DT0012-291299-051-
77 60237188991 NHL_MGC 93
77 RC1-BT0254-271100-121-
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77 603053412F1 NIH_MGC_12
72 AL543472 LTT_NFL006_P1
77 603055968F1 NIH_MGC_12
78 1 QV1-BN0002-061299-039-
25 EST186091 Colon carcin
21 ZV58e07.x1 Soares_test
22 EST186210 Colon carcin
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24 EST186210 Colon carcin
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26 EST1862323F1 NIH_MGC_53
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36 QV4-ST0212-120100-075-

36 603051712F1 NIH_MGC_12

30 6033051712F1 NIH_MGC_91

31 601371509F1 NIH_MGC_5

37 1f23a08.y1 Melton Norm
EST187946 HCC cell li
EST039 Human hepatoce
EST187482 Colon carci
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                                                                                   Align seg
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                                                                                                                                                                                             Ratio: 1.000
Percent Similarity: 100.000
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gb_est1:AA316967
gb_est1:AA315116
gb_est1:AA315166
gb_est1:AW166169
gb_est2:BG501149
gb_est2:BF680021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                              /organism="Homo Sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4806679"
/clone="IMAGE:4806679"
/clone="IMAGE:4806679"
/tissue_type="adenocarcinoma"
/lab_host="DH1DB (T1 phage-resistant)"
/lab_host="DH1DB (T1 phage-resistant)"
/lab_host="brill (ggccgctcteyerc); Site_2: Sill (ggccattatggcc); Site_1: Sill (ggccattatggcc); Site_2: Sill (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ATTCTAGAGGCCGACATATAGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGCGGCCGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
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1.1e-120
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AA315115 EST187838 Colon car
AA315166 EST186963 HCC cell
AW166169 xf46b06.xl NCI_CGAP
BG501149 602546389F1 NIH_MGC
BF680021 602154740F1 NIH_MGC
BF680376 602154161F1 NIH_MGC
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                                                                                                                                                                                HCGP http://www.ludwig.org.br/ORESTES
The FAPESP/LICR Human Cancer Genome Pu
Unpublished (1999)
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.p17t1=QV4&t2=QV4-ST0212-
120100-075-e10&t3=2000-01-12&t4=1)
                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 689)
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                                                                          Tel: +55-11-2704922
Fax: +55-11-2707001
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TCGTCTCTATGCTTACGAACCTGCAGATACAGCTCTGTTGCTTGACAACA
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/clone_lib="ST0212"
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                                                                                      29 gValAlaMetGluLysIleProValSerAlaPheLeuLeuValAlaL 46
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                                                                                                                                 2 CCGCATCCTAGCCGCCGACTCACACAAGGCAGGTGGGTGAGGAAATCCAG
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                                               AGTTGCCATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCC
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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High quality sequence stop: 624.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Plate: LLAM11504 row: h column:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                   194.00
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/db_xref="taxon:9606"
/clone="IMAGE:5201331"
/clone_lib="NIH_MGC_122"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B"
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E:5201331 5',
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 nLysLeuAlaGluGlnPheValLeuLeuAsnLeuValTyrGluThrThrA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 ProHisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleGl 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 TCTCCTACACTCTGGCCAGAGATACCACAGTCAAACCTGGAGCCAAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 AspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnAr 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 CCACACAGTCAAGCTTTAAAGAAAGTGTTTGCTGAAAATAAAGAAATCCA
                                                                                        source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352 GAAATTGGCAGAGCAGTTTGTCCTCCTCAATCTGGTTTATGAAACAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 erLysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGluCys 112
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                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10186 row: o column: 08
                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 750)
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                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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                                                                                                                              quality sequence stop:
                                                                                        1. .750
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/clone="IMAGE:4431583"
/clone_lib="NIH_MGC_91"
                                                                                                          Socation/Qualifiers
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Consortium

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Hominidae;

Euteleostomi;

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EST 06-FEB-2001 E:4431583 5',

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LOCUS BE748141
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ORIGIN
                                                          seq_name: gb_est2:BE748141
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                                                                                                                                                                                                                                           181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 AAGGACTCTCGACCCAAACTGCCCCAGACCCTCTCCAGAGGTTGGGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 hrSerAsnLysProLeuMetIleIleHisHisLeuAspGluCysProHis 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 ProSerArgArgLeuThrGlnGlyArgTrpValArgLysSerArgValAl 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   yrThrLeuAlaArgAspThrThrValLysProGlyAlaLysLysAspThr 64
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                                                                                                                                                                                                                                                                                 TCTCTGACAGTTAGAGCCGATATCACTGGAAGATATTCAAATCGTCTCTA 514
                                                                                                                                                                                                                                                                                                                                                                      ACCITICTCTGATGGCCAGTATGTCCCCAGGATTATGTTTGTTGACCCA 464
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                                                                                                                               laLeuLysLeuLeuLysThrGlu 205
                                                                                                                                                                                              TGCTTACGAACCTGCAGATACAGCTCTGTTGCTTGACAACATGAAGAAAG
                                                                                                                                                                                                                  rAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysA 198
                                                                                                                                                                                                                                                                                                        SerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeuTy 181
                                                                                                                                                                                                                                                                                                                                                                                             CTCTCAAGTTGCTGAAGACTGAA
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/lab_host="nHl0B (phage:resistant)"
/note="Organ: prostate; vector: pcMv-SPORT6; Site_1: NotI;
/note="Organ: prostate; vector: pcMv-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                            31 aMetGluLysIleProValSerAlaPheLeuLeuLeuValAlaLeuSerT 48
                                                                                                                                               Quality:
Ratio:
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 689)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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//clone="IMAGE:383837"
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/tissue_type="from acute myelogenous leukemia"
/lab_host="DH10B (TI phage-resistant)"
/lab_host="DH10B (T
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                                                                                                                                                                                    Fax: 617-495-050, Email: dmelton@biohp.harvard.edu
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing
Library was constructed by Dr. Douglas Melton DNA sequencing
Washington University Genome Sequencing Center For informatic
Washington University Genome Sequencing Security S
                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Endocrine Pancreas Consortium Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Aven MA 02138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Other_ESTs: if23a08.x1
                                                                                                                                                                                                                                                                                                                                                                        Tel: 617-495-1812
Fax: 617-495-8557
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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, Jackson,Y. and Bowers,Y.
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Location/Qualifiers
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laArgAspThrThrValLysProGlyAlaLysLysAspThrLysAspSer
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                   ValArgAlaAspIleThrGlyArgTyrSerAsnArgLeuTyrAlaTyrGl 184
                                                                                                                                                                                                                                           eTrpThrG1nThrTyrG1uG1uA1aLeuTyrLysSerLysThrSerAsnL 101
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                                                                                 CTGATGGCCAGTATGTCCCCAGGATTATGTTTGTTGACCCATCTCTGACA
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/dev_stage="Adult"
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/sex="Both"
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                                                                                                                              laArgAspThrThrValLysProGlyAlaLysLysAspThrLysAspSer 67
                                                                                                                                                                           AATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCCCTCTCCTACACTCTGG 120
                                                                                                                                                                                          sIleProValSerAlaPheLeuLeuLeuValAlaLeuSerTyrThrLeuA 51
                                                                                                                                                                                                                                          CGACTCACACAAGGCAGGTGGGGTGAGGAAATCCAGAGTTGCCATGGAGAA
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AW956284 AW956284
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Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C.,
, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 3528
Fax: 301 838 0208
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP
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1 (bases 1 to 948)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: image.llnl. Plate: LLCM795 row: d column: 17 High quality sequence stop: 748.
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/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: xhoI; Site_2: FoorI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5; cloned into EcoRI/XhoI sites using the following 5; adaptor: GGCACCAAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of the laboratory of the laborator
                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3942112"
/clone_lib="NIH_MGC_7"
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                                              ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLe 137
                                                                                                               etIleIleHisHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120
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uLeuAsnLeuValTyrGluThrThrAspLysHisLeuSerProAspGlyG
                                                                                                TGATTATTCATCACTTGGATGAGTGCCCACACAGTCAAGCTTTAAAGAAA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM9574 row: 1 column: 17 High quality sequence stop: 723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
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/lab_host="DHIOB (phage-resistant)"
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo d
Average insert size 1.8 kb. Library constructed by Li
Technologies. "
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Plate: LLAM10467 row: i column:
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Tissue Procurement: DCTD/DTP
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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/note="Organ: prostate; Vector: pcMV-SPORT6; Site_1: Not
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies
Note: this is a NIH_MGC Library."

194 c 189 g 212 t 1 others
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/clone="IMAGE:4539353"
/clone_lib="NIH_MGC_91"
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                                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 751)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections (1988)
                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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BG386151
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cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (CDNA Sequencing Senter DNA Sequencing Senter Clone distribution: MGC clone distribution informations of the context of the con
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Hominidae;

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ArgLeuTyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMe 195
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Plate: LLCM1307 row: b column: 09
High quality sequence stop: 672.
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Tissue Procurement: ATCC
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/site_2: EcoRI; CDNA made by oligo-dT priming.
/site_2: EcoRI; CDNA made by oligo-dT priming.
/site_3: CDNA mad
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                                                                                                                                                                     cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM1877 row: i column: 16 High quality sequence stop: 792. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 797)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
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Mammalia; Eutheria; Primates;
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/db_xref="taxon:9606"
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/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
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sapiens cD
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                                       ACCESSION
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                                     mRNA sequence.
BM006784
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129 281

REFERENCE

JOURNAL

bp mR sapiens

cDNA clone

mRNA

linear

IMAGE:5420836 5',

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Quality: 178.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                               CGTCTCTATGCTTACGAACCTGCAGATACAGCTCTGTTGCTTGACAACAT
                                                                                                                               ArgLeuTyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMe
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gb_est2:BM006784
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                                                                                                                                                     sSerLysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGluC 112
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                                             GCCCACACAGTCAAGCTTTAAAGAAAGTGTTTGCTGAAAATAAAGAAATC
                                                                   ysProHisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIle 128
                                                                                                                                   ATCCAAGACAAGCAACAAACCCTTGATGATTATTCATCACTTGGATGAGT 280
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert St
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA Synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plate: LLCM1877 row: j column: High quality sequence stop: 781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MCC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          numan
                                                                                                                                                                     278
                                                                                                                                                                                                                                 /tissue_type="ductal carcinoma, cell line"
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/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA swnthesia before
100.000
                                                                                                                                                              of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NHT_MGC Library."

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/clone_lib="NIH_MGC_110"
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Percent Identity:
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                                                                                                                                                  ArgLeuTyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMe 195
                                                 TTGACCCATCTCTGACAGTTAGAGCCGATATCACTGGAAGATATTCAAAC
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Database: Issued_Patents_NA:*
Database sequences: 383533
Database length: 122816752
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2.9e-47
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alignment_block:
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                                                             Percent Similarity:
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                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/024,347
FILING DATE: 23-AUG-1996
ATTORNEY_AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
                                                                                                 FEATURE:
NAME/KEY:
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                                                                                                                                                                                                     MOLECULE TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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STATE: DC
COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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US-08-916-576B-1

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Gaps: : Identity:

100.000

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CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-10-04
NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04
NUMBER: OF SEQ ID NOS: 182
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                                                                                                                                                                                                                                                                     Sequence 61, Application US/09247155A Patent No. 6312922 GENERAL INFORMATION:
                                                                                                                                                                                      APPLICANT: Dumas Milne Edwards, Je APPLICANT: Duclert, Aymeric APPLICANT: Bougueleret, Lydie TITLE OF INVENTION: Complementary FILE REFERENCE: GENSET 021A
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|CTCTCAAGTTGCTGAAGACTGAATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uAlaGluGlnPheValLeuLeuAsnLeuValTyrGluThrThrAspLysH 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yrThrLeuAlaArgAspThrThrValLysProGlyAlaLysLysAspThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeuTy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCAGAGCAGTTTGTCCTCCTCAATCTGGTTTATGAAACAACTGACAAAC
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US-09-674-266A-181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 51..575
FEATURE:
NAME/KEY: $19_Peptide
LOCATION: 51..110
OTHER INFORMATION: Von Heijne matrix
'OTHER INFORMATION: score 11.2
OTHER INFORMATION: seq AFILLVALSYTLA/RD
FEATURE:
NAME/KEY: polyA_signal
LOCATION: 1653..1658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to:
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NAME/KEY: polyA_site
LOCATION: 1674..1689
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                                                                                                                                                                                                                                       GlnLysLeuAlaGluGlnPheValLeuLeuAsnLeuValTyrGluThrTh
                                                                                                                                                                                                                                                                                                    ysProHisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIle
                                                                                                                                                                                                                                                                                                                                                                 sSerLysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGluC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ArgValAlaMetGluLysIleProValSerAlaPheLeuLeuLeuValAl
                                                                                             TTGACCCATCTCTGACAGTTAGAGCCGATATCACTGGAAGATATTCAAAT
                                                                                                                                                                                                                         CAGAAATTGGCAGAGCAGTTTGTCCTCCTCAATCTGGTTTATGAAACAAC
                                                                                                                                                                                                                                                                                      GCCCACACAGTCAAGCTTTAAAGAAAGTGTTTGCTGAAAATAAAGAAATC
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tLysLysAlaLeuLysLeuLeuLysThrGluLeu
                                                                                                                                                          TGACAAACACCTTTCTCCTGATGGCCAGTATGTCCCCCAGGATTATGTTTG
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Gaps: 0
Percent Identity: 100.000
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from: 1

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-916-576B-35
                                                                                                                                                                                                                                                            US-09-674-266A-181 x US-08-916-576B-35
                                                                                                                                                                                                                                                                                                                 Quality: 107.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                    Align seg 1/1 to: US-08-916-576B-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence 35, Application US/08916576B Patent No. 6171816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202) 371-254 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0500001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 386 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 11
MOLECULE TYPE:
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                                                                                                                                                             82 GlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrLysSerLysTh
                                                                           98 rSerAsnLysProLeuMetIleIleHisHisLeuAspGluCysProHisS 115
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erGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleGlnLysLeu 131
                                                                                                                                      CAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAAATCCAAGAC 113
                                                           AAGCAACAAACCCTTGATGATTATTCATCACTTGGATGAGTGCCCACACA
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EBNER, REINHARD
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202) 371-2540
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                                                                                                                          alignment_block:
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                                                                                                                                                                                                                                                                    ; TOPOLOGY: US-09-040-984-78
                                                                                                         US-09-674-266A-181 x US-09-040-984-78
                                                                                                                                                             Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 78, Application US/09040984 Patent No. 6210883
                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION UNMEER: US/09/040,984
FILING DATE: 18-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Reed, Steven G.
APPLICANT: Wang, TongTong
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
TITLE OF INVENTION: OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 sLeuSerProAspGlyGlnTyrValProArgIleMetPheValAspProS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               314 CTCTGACAGTTAGAGCCGATATCACTGGAAGATATTCAAATCGTCTCTAT 363
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CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                    LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: SEED and BERRY LLP STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 206-282-6031
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                                                                                                                                                                                              Quality:
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                                                                      US-09-040-984-78
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                                                                                                                                                             Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Pa
SEQ ID NO 78
LENGTH: 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 78, Application US/09123912A
patent No. 6312695
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
FILE REFERENCE: 210121.455C1
                                                                                       LOCATION: (563)
OTHER INFORMATION: Where n
NAME/KEY: modified_base
LOCATION: (657)
OTHER INFORMATION: Where n
NAME/KEY: modified_base
LOCATION: (660)
OTHER INFORMATION: Where n
NAME/KEY: modified_base
LOCATION: (703)
OTHER INFORMATION: Where n
NAME/KEY: modified_base
LOCATION: (708)
OTHER INFORMATION: Where n
NAME/KEY: modified_base
LOCATION: (708)
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OTHER INFORMATION: where n NAME/KEY: modified_base LOCATION: (711)
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LOCATION: (309)
OTHER INFORMATION: where n
NAME/KEY: modified_base
LOCATION: (492)
OTHER INFORMATION: where n
NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/123,912A CURRENT FILING DATE: 1998-07-27 PRIOR APPLICATION NUMBER: 09/040,802 PRIOR FILING DATE: 1998-03-18 NUMBER OF SEQ ID NOS: 114
                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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; OTHER INFORMATION: Where US-09-123-912-78
                                                                                                        seq_documentation_block:
                                                                                                                                 seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-221-298-32
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US-09-674-266A-181 x US-09-123-912-78
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Quality:
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                                                              Sequence 32, Application US/09221298 Patent No. 6284241 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOUNDS AND METHODS
TITLE OF INVENTION: OF COLON CANCER
FILE REFERENCE: 210121.471
FILE REFERENCE: 210121.471
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OTHER INFORMATION: Where
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alignment_block:
US-09-674-266A-181 x US-09-221-298-32
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; ORGANISM: Human
US-09-221-298-32
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; Sequence 149, Applicat
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Quality:
                                                                                                                       NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
SEQ ID NO 149
LENGTH: 940
TYPE: DNA
ORGANISM: Homo sapiens
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NUMBER OF SEQ ID NOS: 112
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence 149, Application US/09247155A Patent No. 6312922 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: GENSET.021A
CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT FILING DATE: 1999-02-09
                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: 60/074,121 EARLIER FILING DATE: 1998-02-09 EARLIER APPLICATION NUMBER: 60/081,563 EARLIER FILING DATE: 1998-04-13 EARLIER APPLICATION NUMBER: 60/096,116 EARLIER FILING DATE: 1998-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dumas Milne Edwards, Jean-Baptiste APPLICANT: Duclert, Aymeric APPLICANT: Bougueleret, Lydie TITLE OF INVENTION: Complementary DNAS
                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 60/099,273 EARLIER FILING DATE: 1998-10-04
                                                                                                         FEATURE:
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                                                               NAME/KEY: CDS
LOCATION: 177..569
NAME/KEY: sig_peptide LOCATION: 177..236
                                          FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: 482
; OTHER INFORMATION: n=a,
US-09-247-155-149
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: YU, GUO-LIANG
APPLICANT: DILLON, PINTARICK J.
APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
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                                                                               FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                           ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C. STREET: 1100 NEW YORK AVENUE, SUITE 600 CITY: WASHINGTON
                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                     ZIP: 20005-3934
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alignment_block:
US-09-674-266A-181 x US-08-916-576B-36
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Ratio: 1.000
Percent Similarity: 100.000
                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 209, Application US/09030607 Patent No. 6262245
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 373 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 1: MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 GACTCTCGA 159
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                    TELEPHONE:
                                                                                                                                                                                                                                                                                           ZIP: 98104
                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                            CITY: Seattle
STATE: WA
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                                                                                                                                                                                                                                                                                                              USA
   (206) 622-4900
(206) 682-6031
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Percent Identity: 100.000
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-030-607-209
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Quality:
alignment_block:
                                                                                         alignment_scores:
                                                                                                                                               ; ORGANISM: Homo sapien 
US-09-439-313-209
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                                       Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 209,
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Xu, Jiangchun
                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                      Quality:
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Reed, Steven G.
Kalos, Michael
                                                      Ratio:
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Retter, Mark
Solk, John
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Day, Craig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dillon, Davin C
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                                     : 52.00
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1.000
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seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-439-313-209
                                                                                                                                                                 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 209
LENGTH: 159
TYPE: DNA
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Gaps: 0
Percent Identity: 100.000
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alignment_scores:
Quality:
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                                                                                                              ; MOLECULE TYPE: US-08-916-576B-37
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   Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: YU, GU
APPLICANT: DILLON
                                                                                                                                                                                                                                        TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,347
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 CTCTCC 158
                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 ValArgLysSerArgValAlaMetGluLysIleProValSerAlaPheLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: WASHINGTON
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGAGCCAAAAAGGACACAAAGGACTCTCGACCCAAACTGCCCCAGACC 152
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6171816
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                 Ratio:
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DILLON, PATRICK J.
EBNER, REINHARD
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 Percent Identity:
                                                                                                                                                                                                                                                                                                                    1488.0500001
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                                      Length:
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alignment_scores:
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US-09-674-266A-181 x US-08-916-576B-37
                                                          US-08-916-576B-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: YU, GUO-LIANG
APPLICANT: DILLON, PATRICK
APPLICANT: EBNER, REINHARD
                                                                                                                                                                  TELEFAX: (202) 371-254
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                        NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 141
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                          STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/024,347 FILING DATE: 23-AUG-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 CATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCCTCTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 CCTAGCCGCCGACTCACACAAGGCAGGTGGGGTGAGGAAATCCAGAGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C. STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158
                                                                                                                                nucleic acid
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                                                                                                                                                    489 base pairs
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                                                                                                                                                                                                            371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PATRICK J.
                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/916,576B
                                                                                                                                                                                                                                                                      1488.0500001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version #1.30
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Ratio: Percent Similarity:

Quality:

38.00 1.000 100.000

Percent Identity:

Length:

38 0 100.000

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alignment_block:
US-09-674-266A-181 x US-08-916-576B-10
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US-09-674-266A-181 x US-08-916-576B-9
                                                                                                 alignment_scores:
Quality:
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                                                                                                                                                                                  US-08-916-576B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                      Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/08916576B Patent No. 6171816
                                                                                                                                                                                                                                                                                                                    TELEFAX: (202) 371-25. INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/024,347 FILING DATE: 23-AUG-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: YU, GUO-LIANG
APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 506 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140
                                                                                                                                                                                                  TOPOLOGY: 1:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 ysAspThrLysAsp 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 aLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAlaLysL 62
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                                                                                                                                                                                                                                                                                                                                                                                             NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1100 NEW CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/916,576B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGAGTTGCCATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGC
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                                                                                                                                                                                                                                                         nucleic acid
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                                                                                                                                                                                                                                                                                                                                        (202) 371-2540
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                                                          Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                               1488.0500001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version #1.30
                                                                                                   Length:
                                                                               Gaps:
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alignment_block:
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                                  US-09-674-266A-181 x US-08-916-576B-38
Align seg 1/1
                                                                                        Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: YU, GUO-LIANG
APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
                                                                                                                                                                                                                                                                                                                       TELEFAX: (202) 371-25. INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,347
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 1:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 136 base pairs
                                                                                                                                                                                                                                                                                                                                                                       NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0500001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 yrGluThrThr 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 LeuAspGluCysProHisSerGlnAlaLeuLysLysValPheAlaGluAs 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 TTGGATGAGTGCCCACACAGTCAAGCTTTAAAGAAAGTGTTTGCTGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                         Quality:
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                                                                                                                                                                                                                                                                  nucleic acid
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                                                                                                      Ratio:
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to: US-08-916-576B-38
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                                                                                      Gaps:
Percent Identity:
 from: 1
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 to: 136
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alignment_scores:
Quality:
Ratio:
Percent Similarity: 1
alignment_block:
US-09-674-266A-181 x US-08-916-576B-5
                                                                                                                                                        ; NAME/KEY:
; LOCATION:
US-08-916-576B-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR EGO ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/08/916 FTLING DATE:

CLASSIFFOR:

LIGHTON NUMBER: US/08/916 FTC.

CLASSIFFOR:

LIOPPY disk

CCLASSIFFOR:

LIOPPY disk

CCLASSIFFOR:

LIOPPY disk

PC - DOS/MS - DOS

COPERATING STATE

PLICATION NUMBER: US/08/916 FTC.

CLASSIFFOR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 146
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,347
FILLING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: YU, GUO-LIANG
APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: WASHINGTON
                                                                                                                                                                                                                                                                           LOCATION:
                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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49.:546
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118..546
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49..117
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                                                    24.00
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